

FIGURE 1

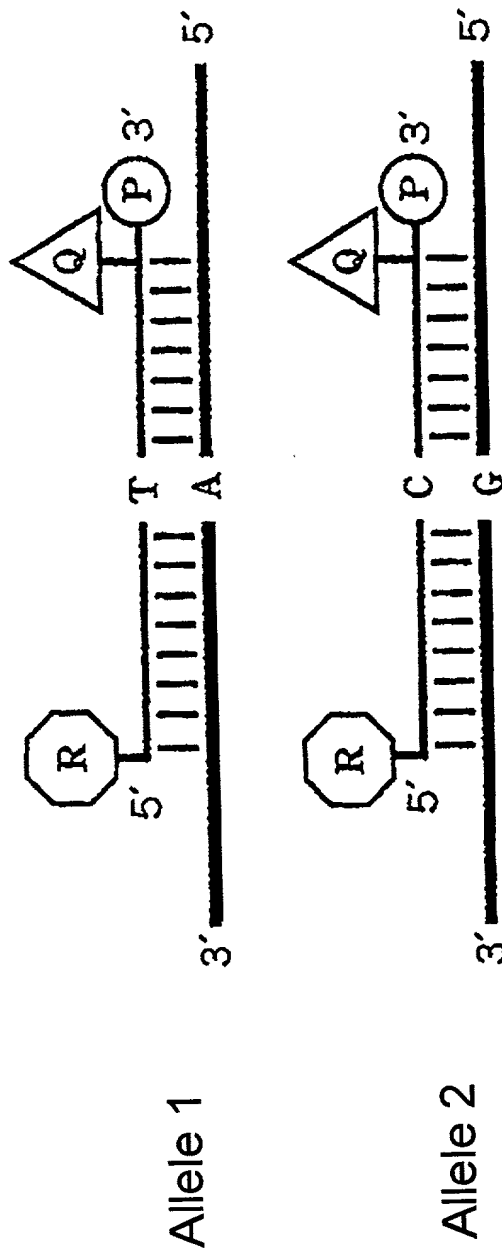


Fig. 302

*L1 cell adhesion molecule (L1CAM)*

Accession No. U52112

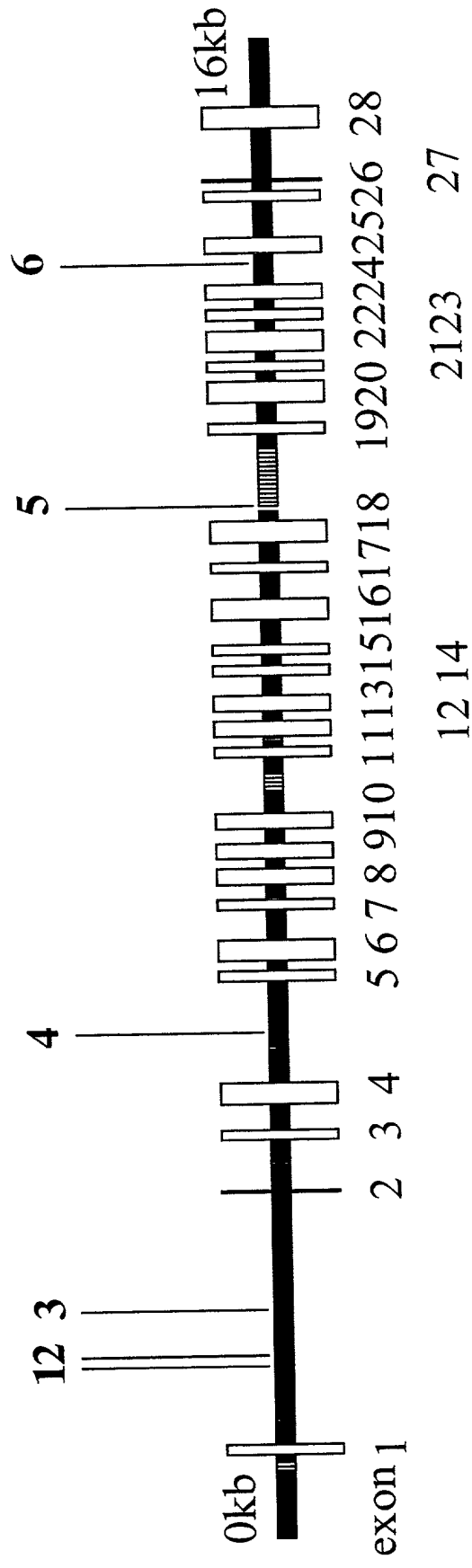


FIGURE 3

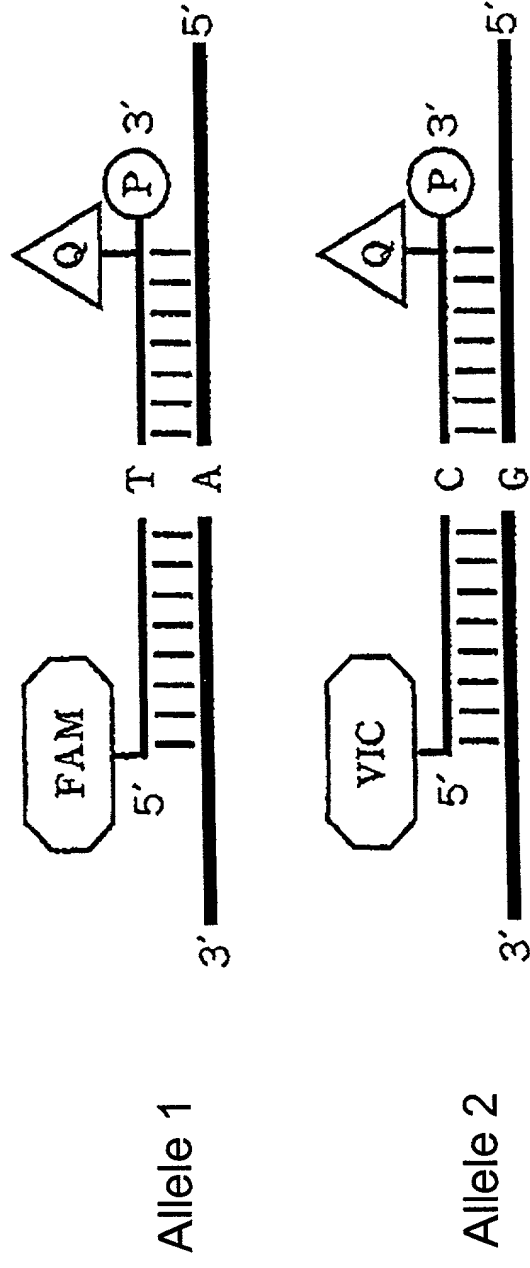


FIGURE 4

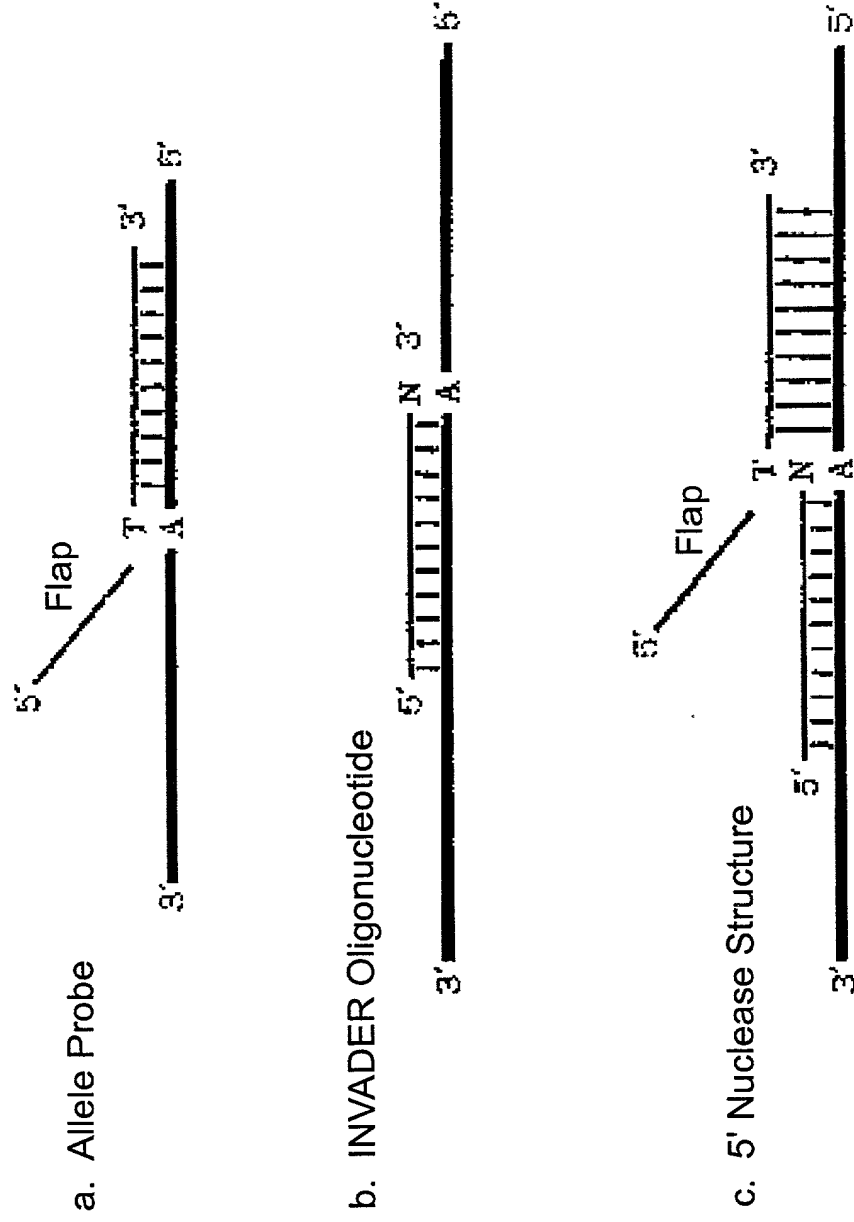




FIGURE 5

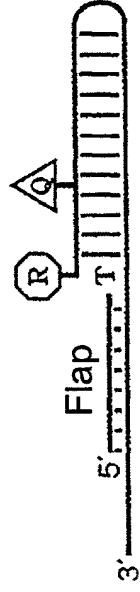


FIGURE 6

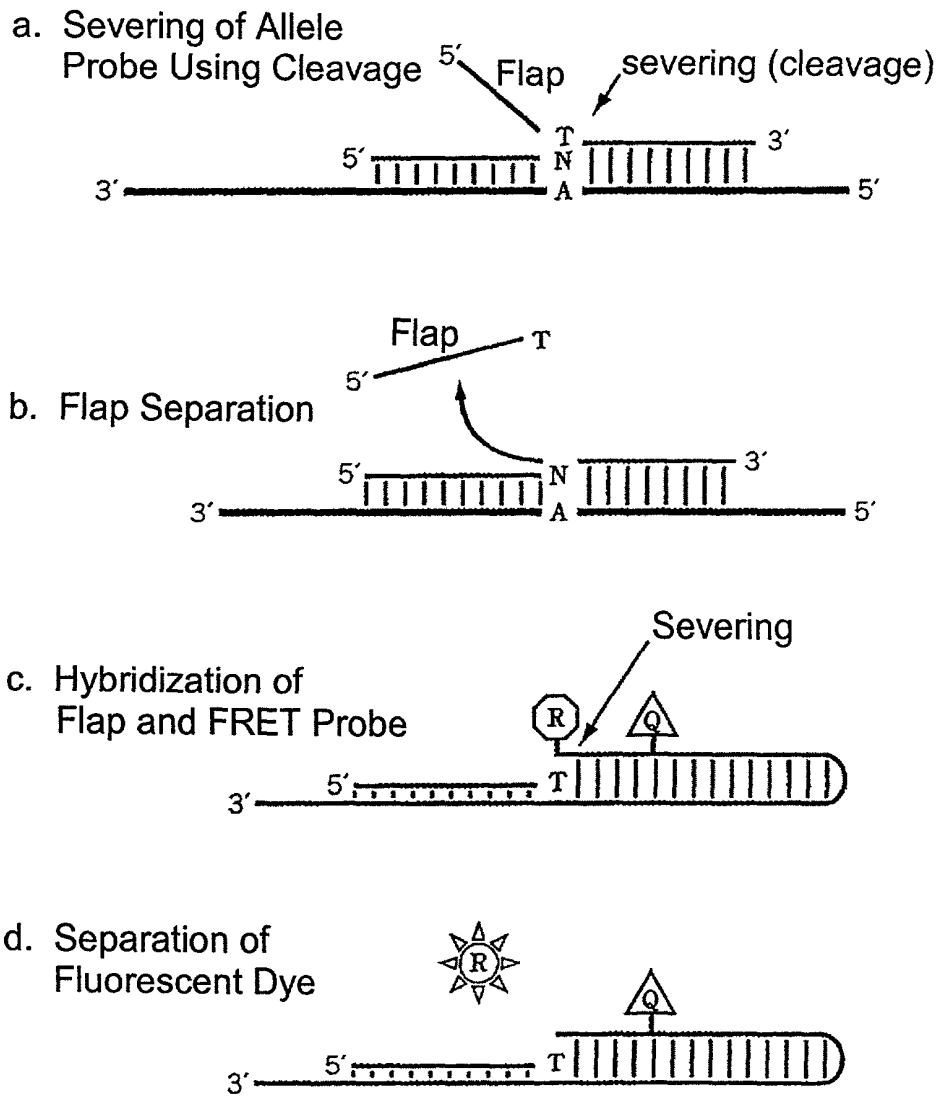


FIGURE 7

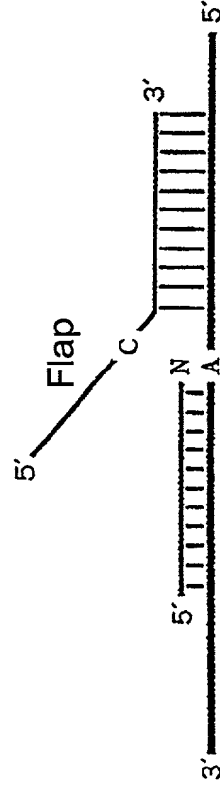
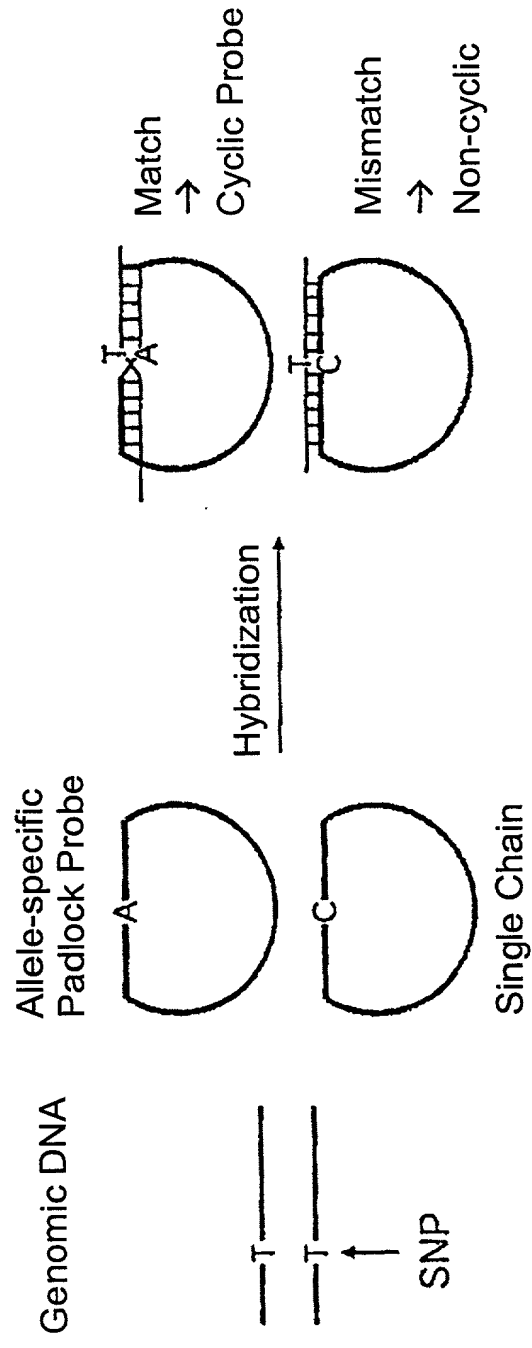


FIGURE 8



*ATP binding cassette, sub-family B, member 2 (ABCB2)*

ACCESSION X66401

FIGURE 9

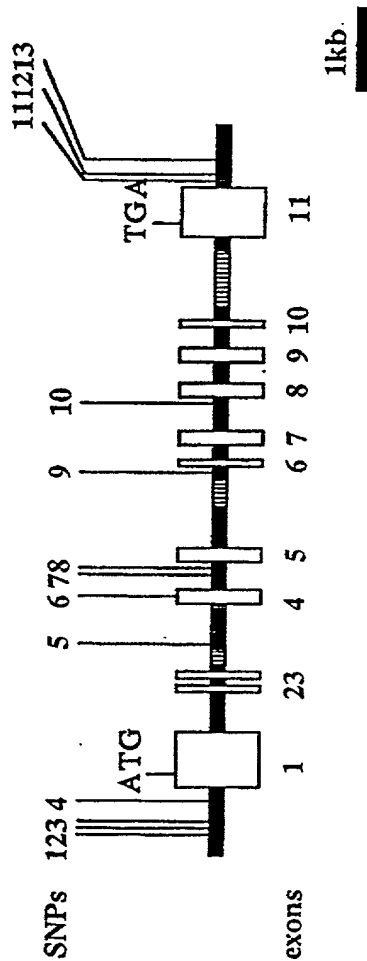


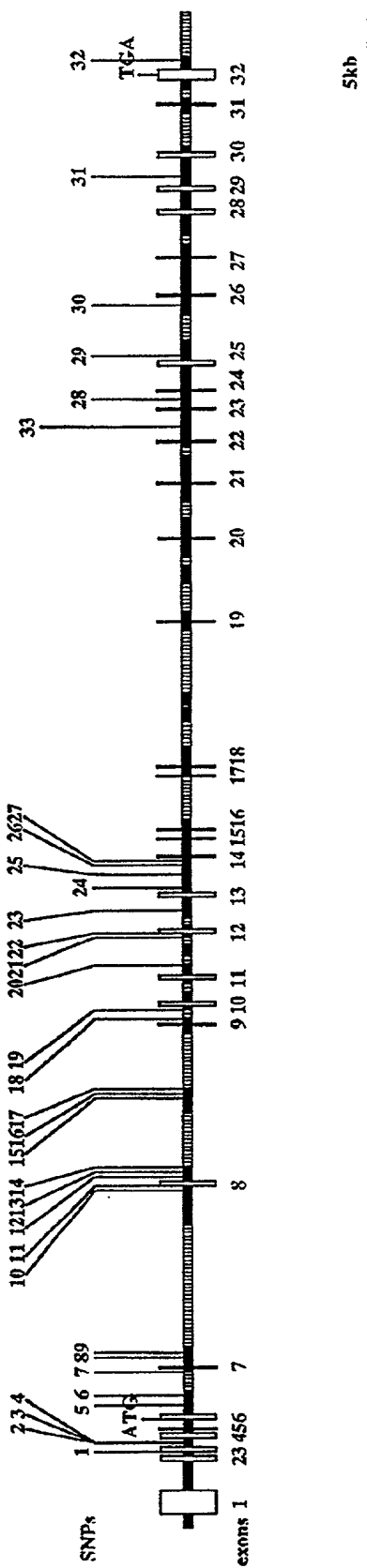
FIGURE 10

*ATP-binding cassette, sub-family B, member 4 (ABCB4)*

ACCESSION AC079591

AC079303

AC005045



*Epoxide hydrolase 1, microsomal (EPHX1)*

ACCESSION AC058782

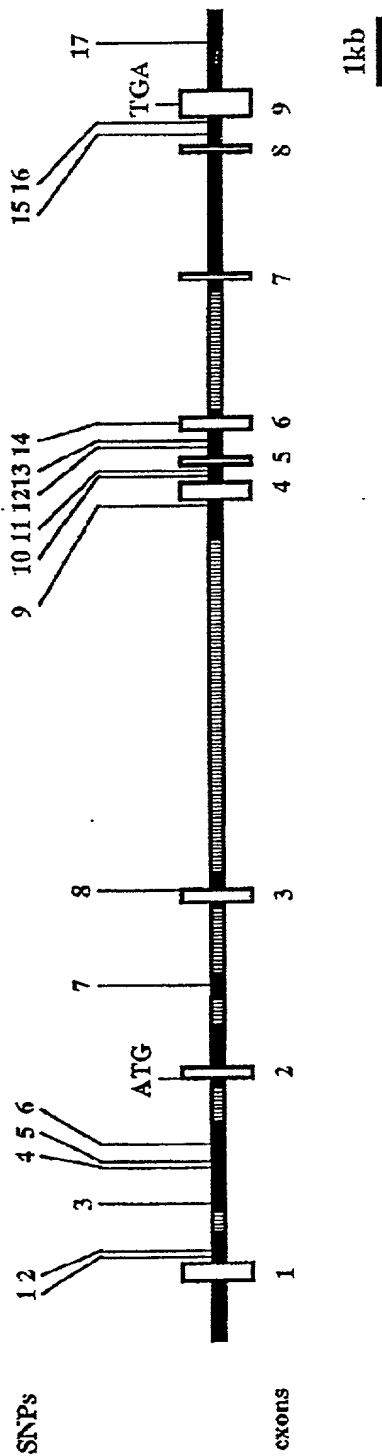
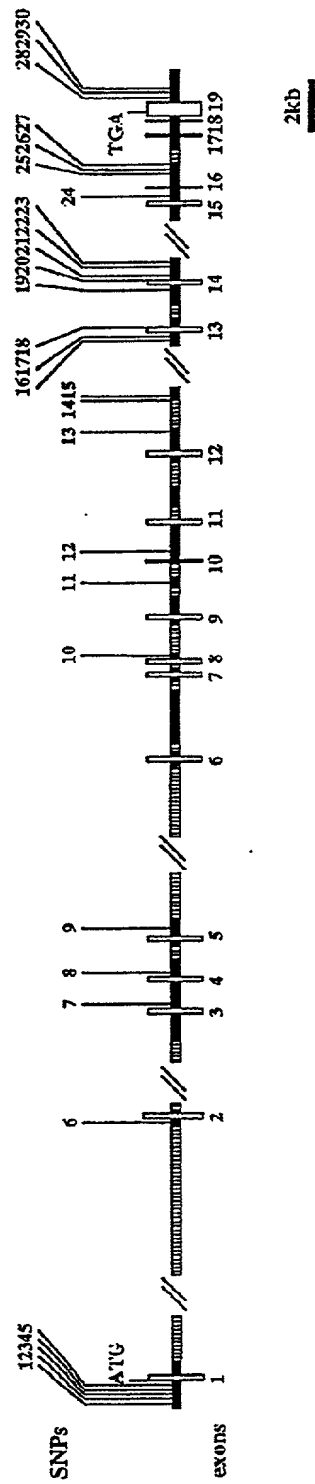


FIGURE 11

FIGURE 12

*Epoxide hydrolase, cytoplasmic (EPHX2)*

ACCESSION AC010856





# *Guanidinoacetate N-methyltransferase ( GAMT )*

ACCESSION NT\_000879

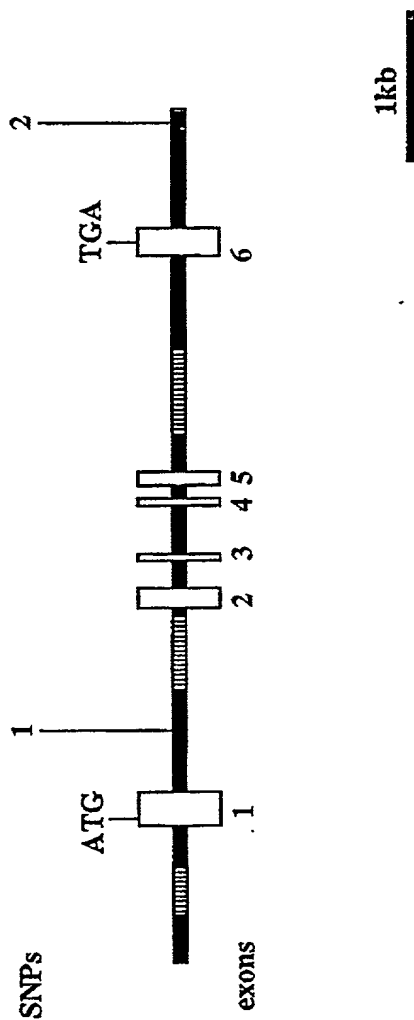


FIGURE 13

Fig. 276

# *Gamma-glutamyltransferase 1 (GGT1)*

ACCESSION D87002.1

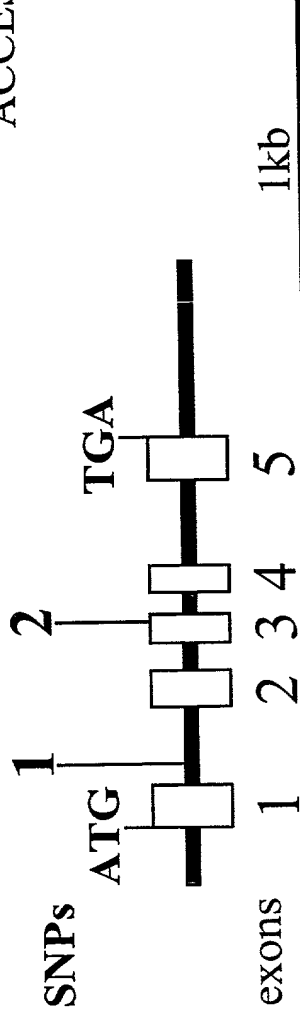
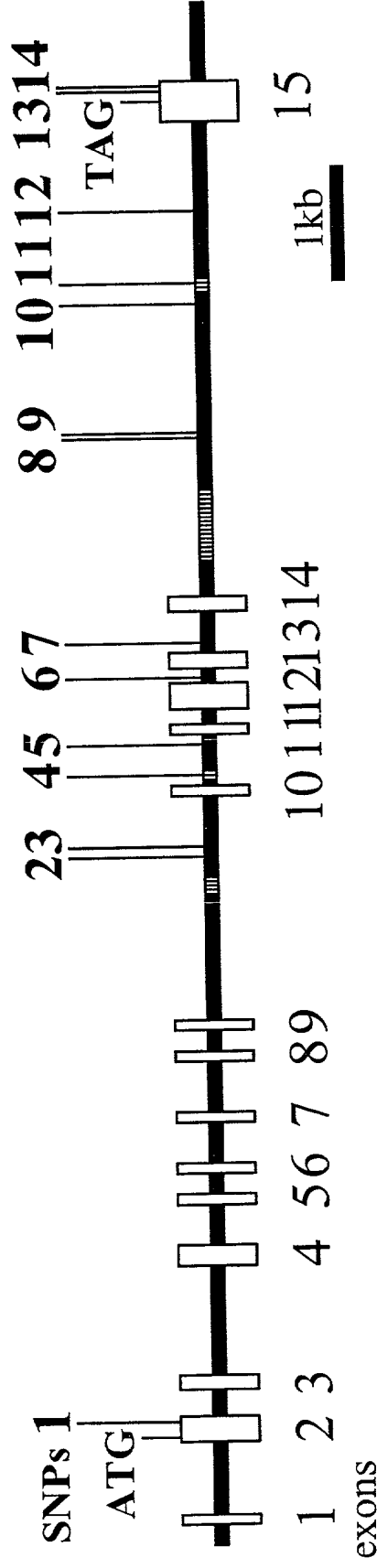


Fig. 277

# *Transglutaminase 1 (TGMI)*

ACCESSION M98447.1



# *Phenylethanolamine N-methyltransferase ( PNMT )*

ACCESSION AC040933

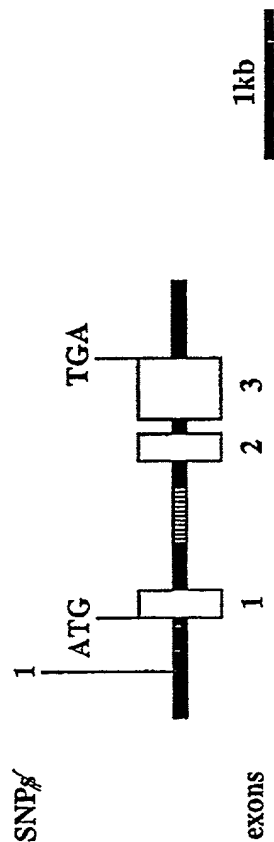


FIGURE 15

ACCESSION A C020558

FIGURE 16

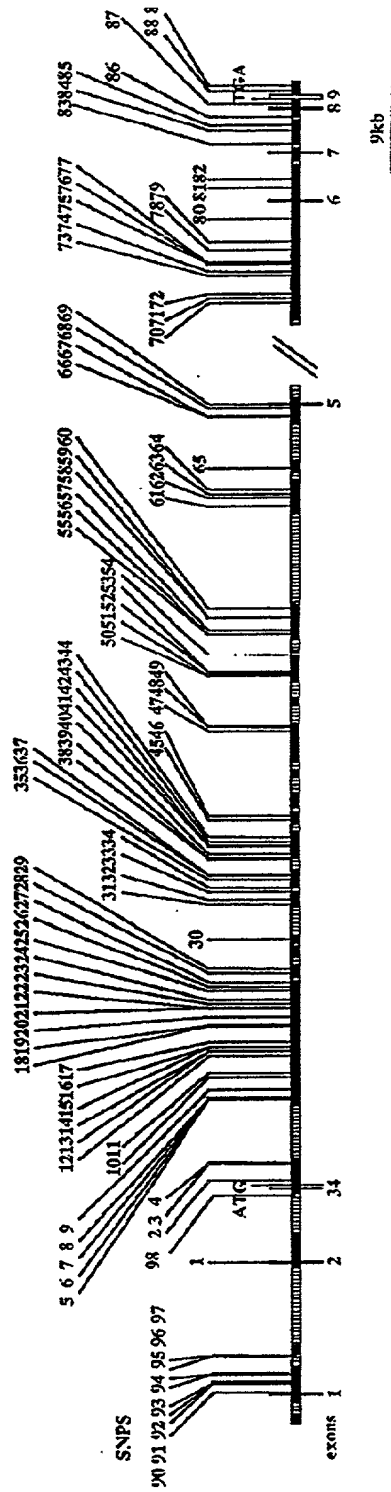


FIGURE 18

*Aldehyde dehydrogenase 5 (ALDH5)*

ACCESSION AL135785

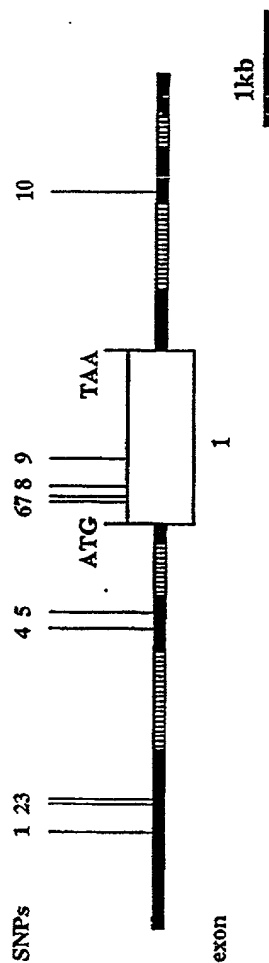
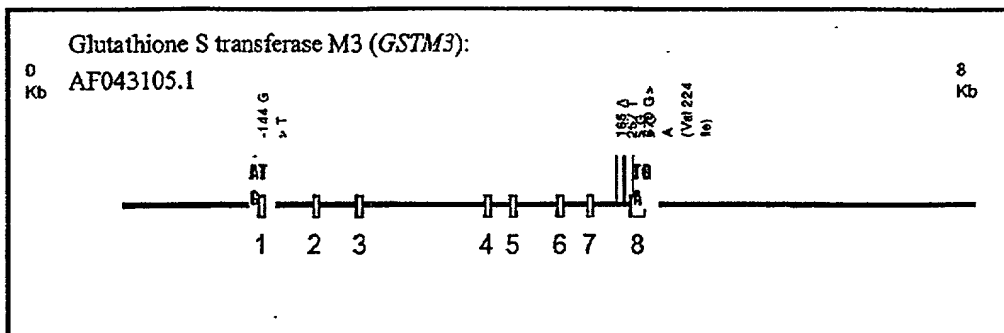


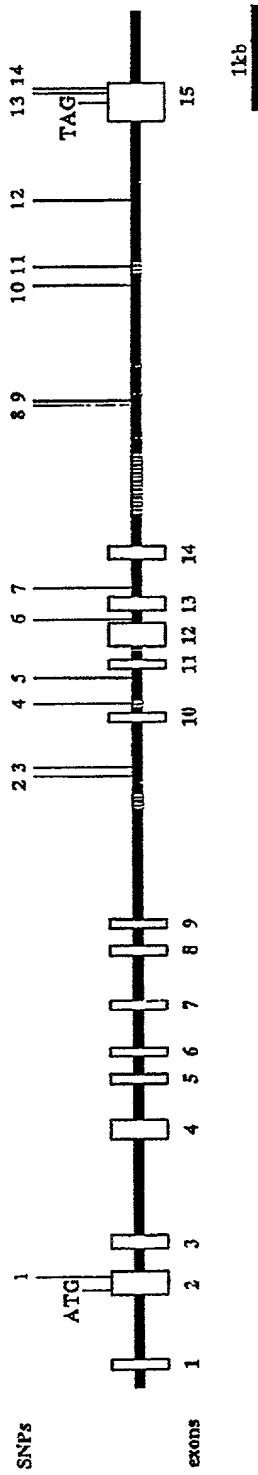
FIGURE 17



*Transglutaminase 1 (TGM1)*

ACCESSION M98447

FIGURE 19



*Gamma- glutamyltransferase 1 ( GGT1 )*

ACCESSION D87002

1kb

FIGURE 21

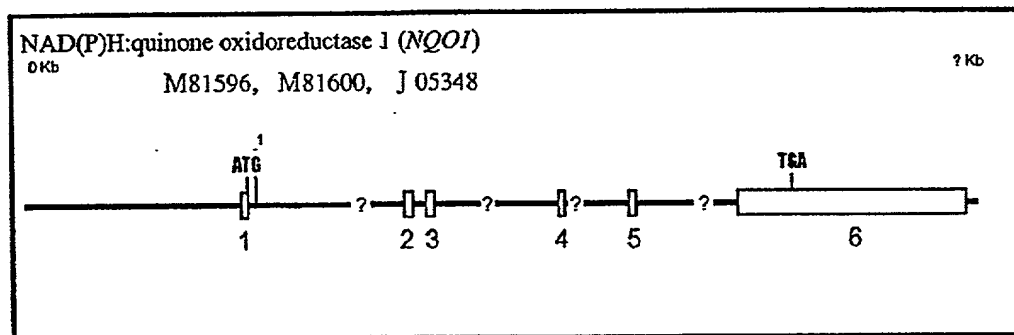


FIGURE 22

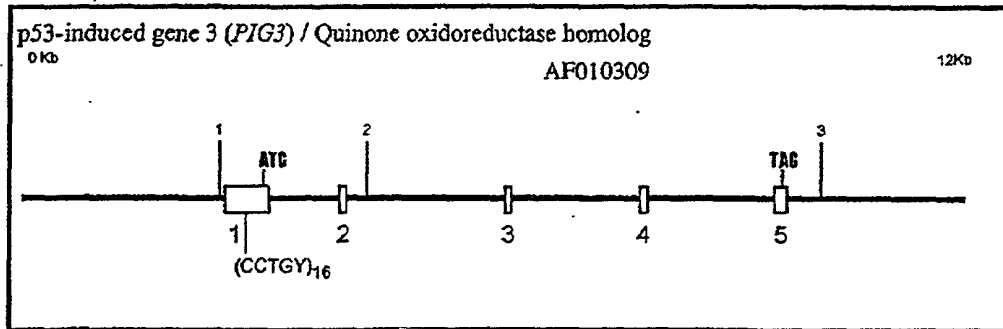


FIGURE 23

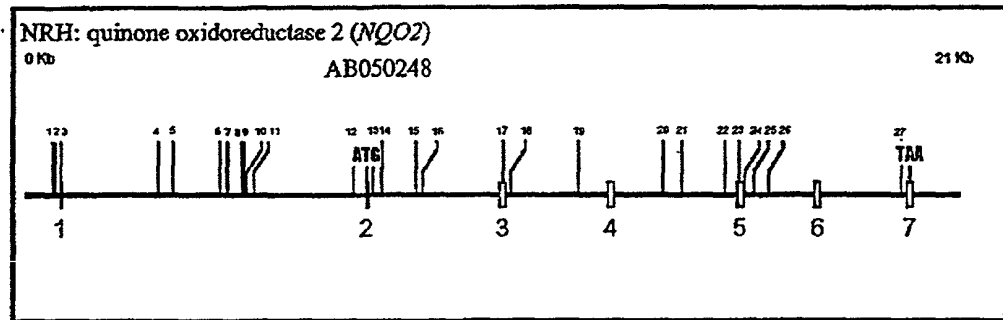


FIGURE 24

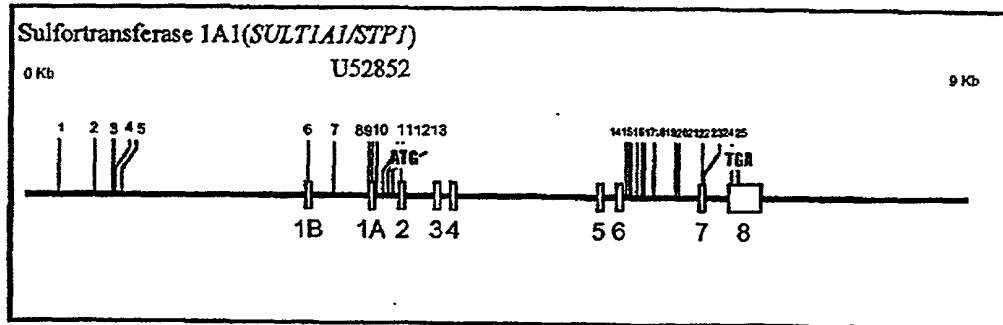


FIGURE 25

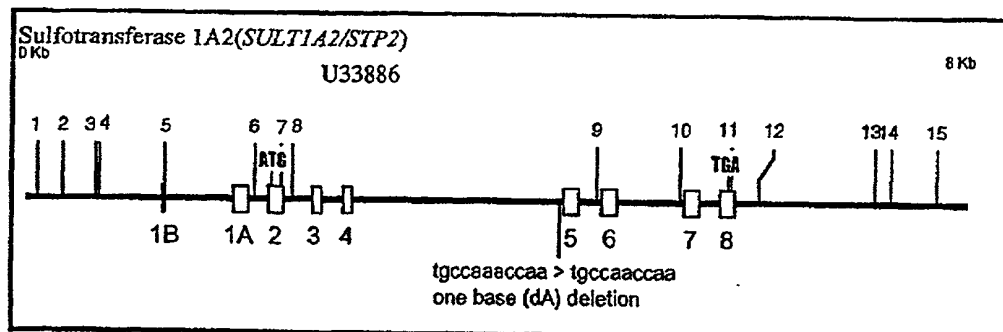




FIGURE 26

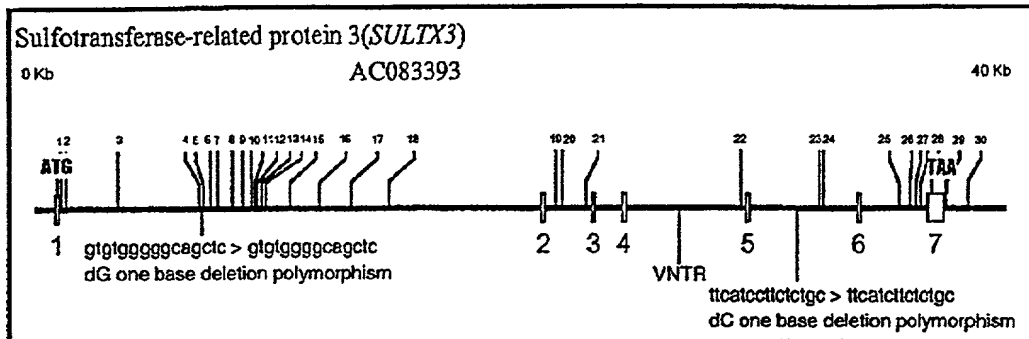


FIGURE 27

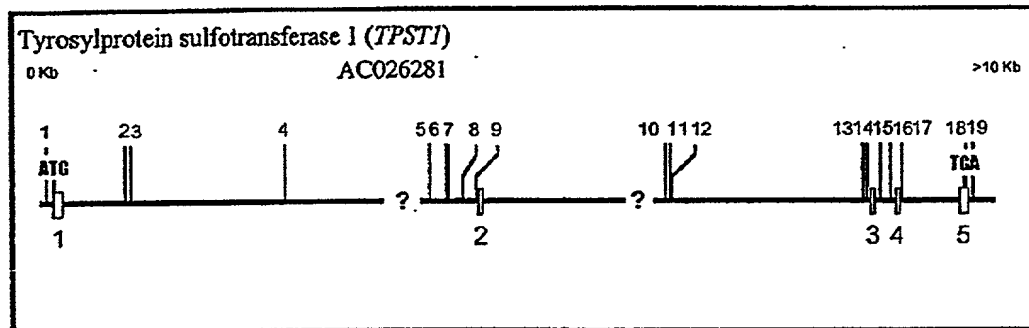


FIGURE 28

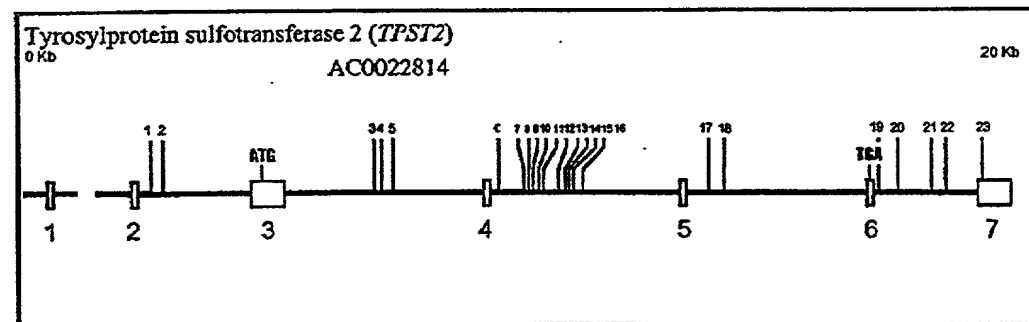


FIGURE 29

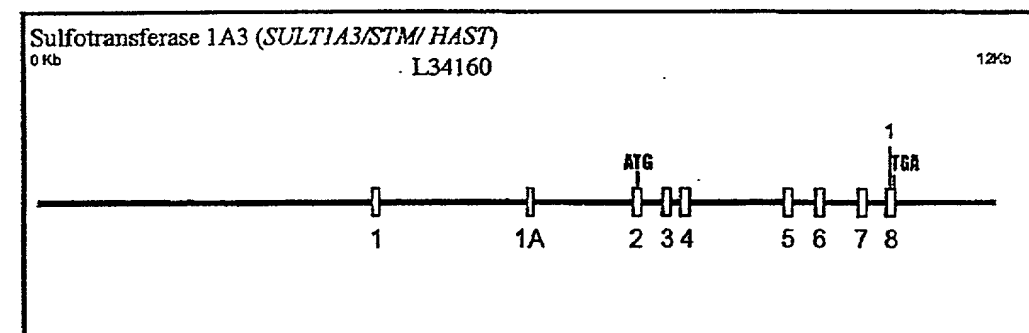
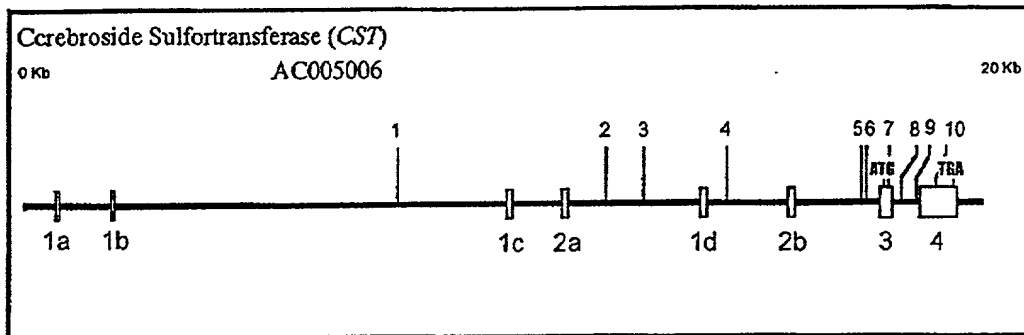


FIGURE 30



[ 3 1 ]

FIGURE 31

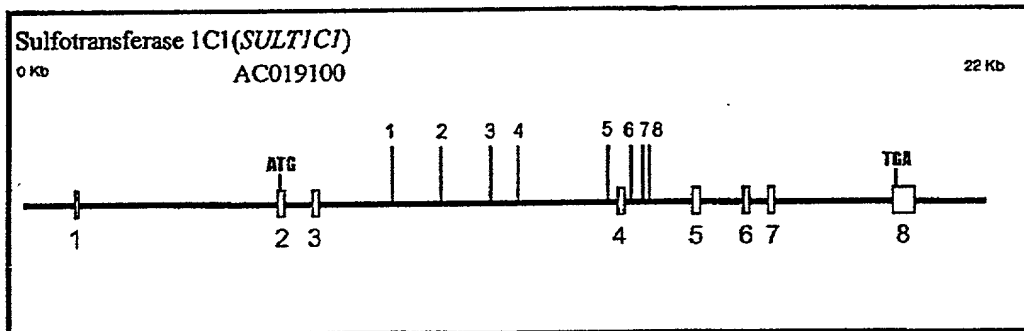


FIGURE 32

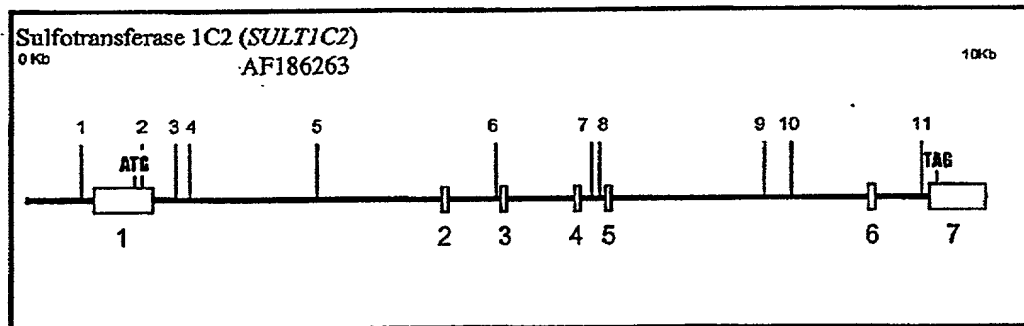
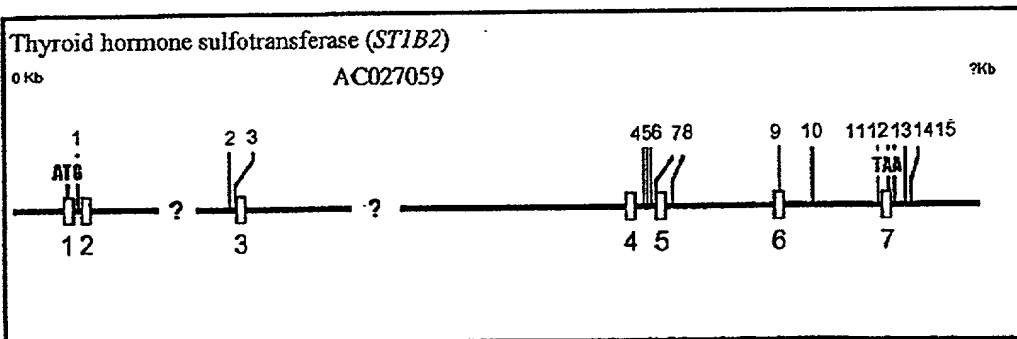


FIGURE 33



# TACCTGCCTC

Observed : G/C  
3' Assay : TACCTGCCTC TTACAGTACC TACCTGCCTA CCTGCCTCTG AGGAGAAACG CTGTAATTAG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_004648.3 (Graphical View of this Entry)  
Chromosome : 1  
map  
Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.  
Position in Sequence : 422012 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_004648.3 20010416\_3  
Amplified region : 421033..422147 in NT\_004648  
size : 1115

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CGAAGAATAT ACTGCTACGG	T

FIGURE 37

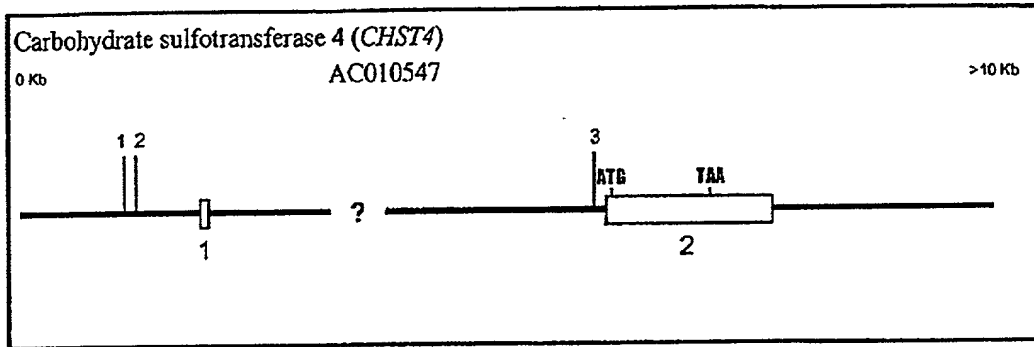


FIGURE 38

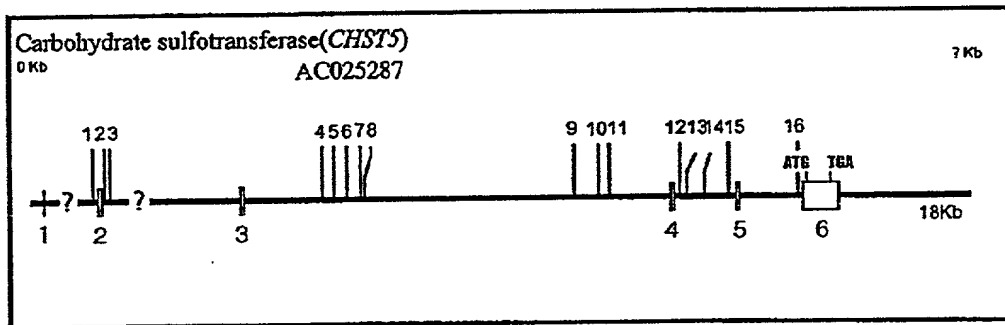


FIGURE 39

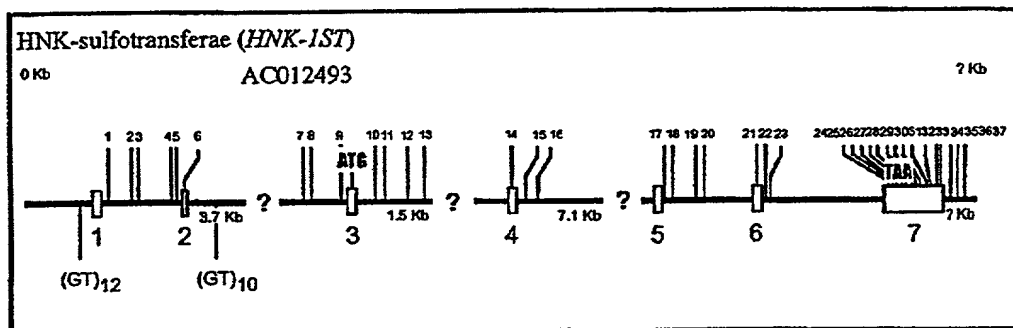


FIGURE 40

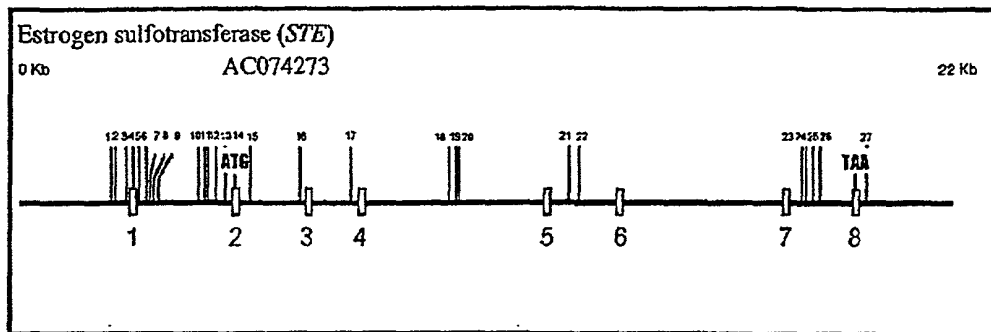


FIGURE 41

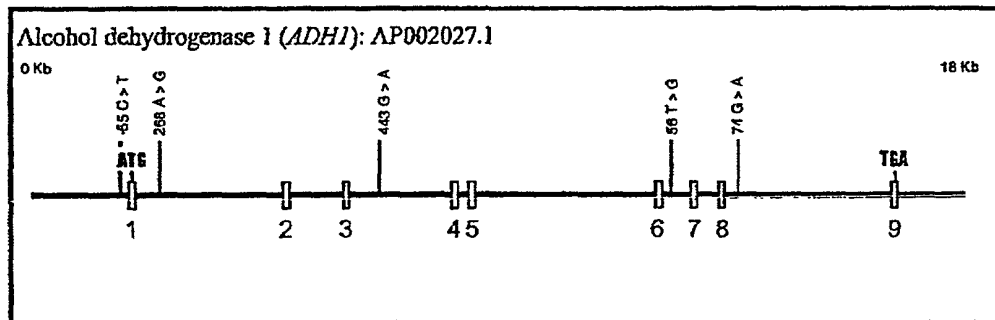


FIGURE 42

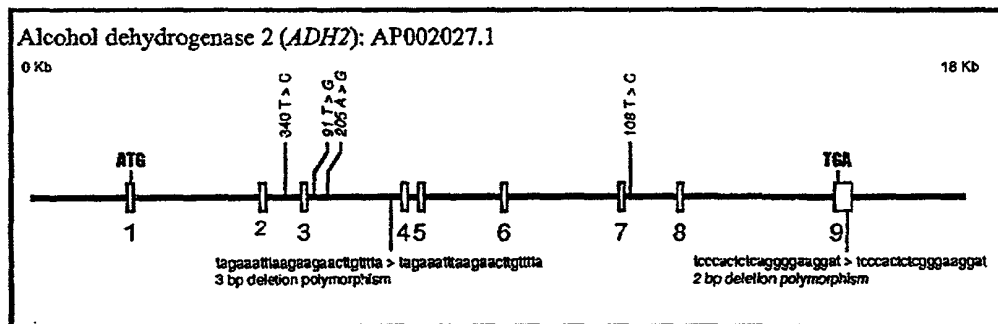


FIGURE 43

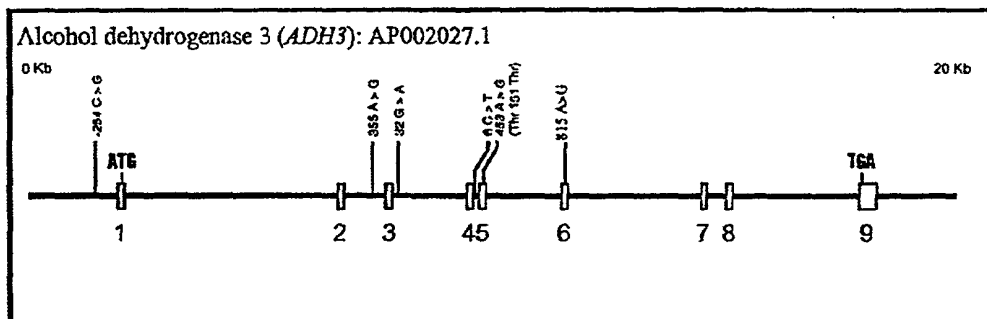


FIGURE 44

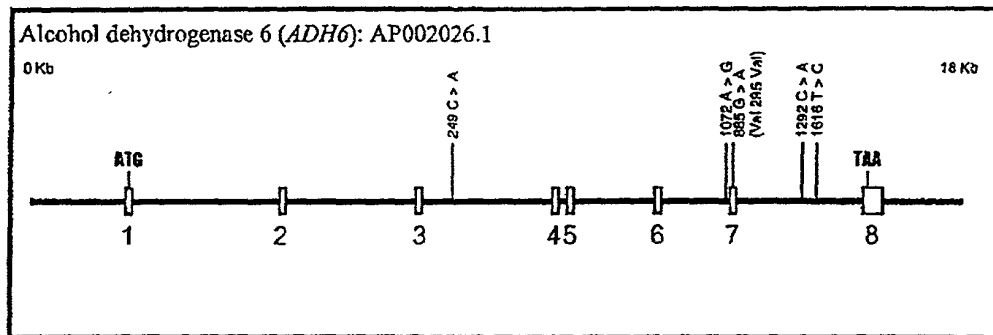


FIGURE 45

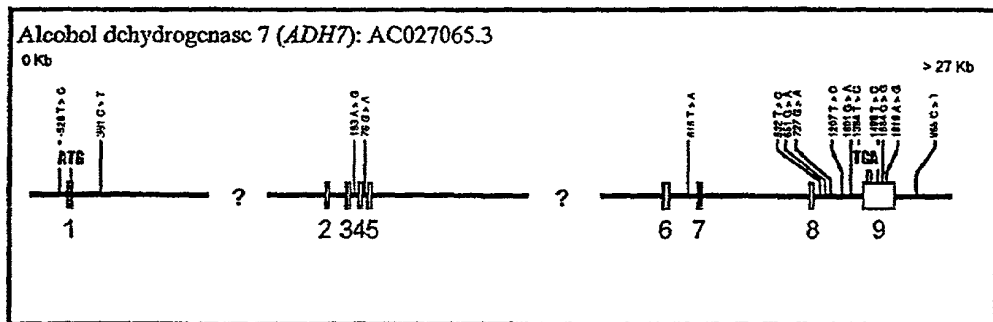
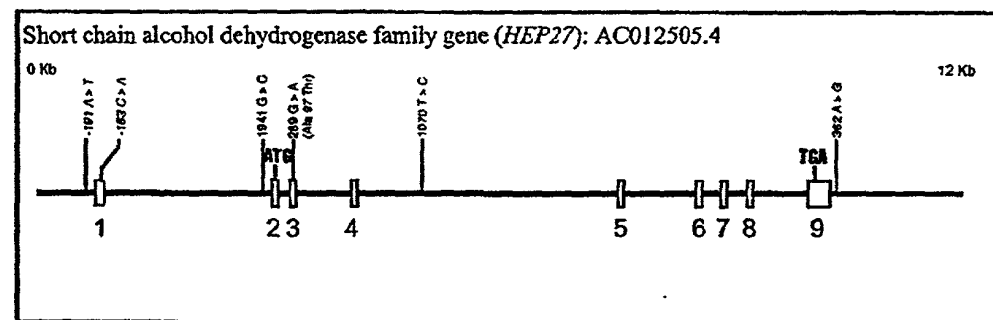


FIGURE 46



*L1 cell adhesion molecule (L1CAM)*

Accession No. U52112

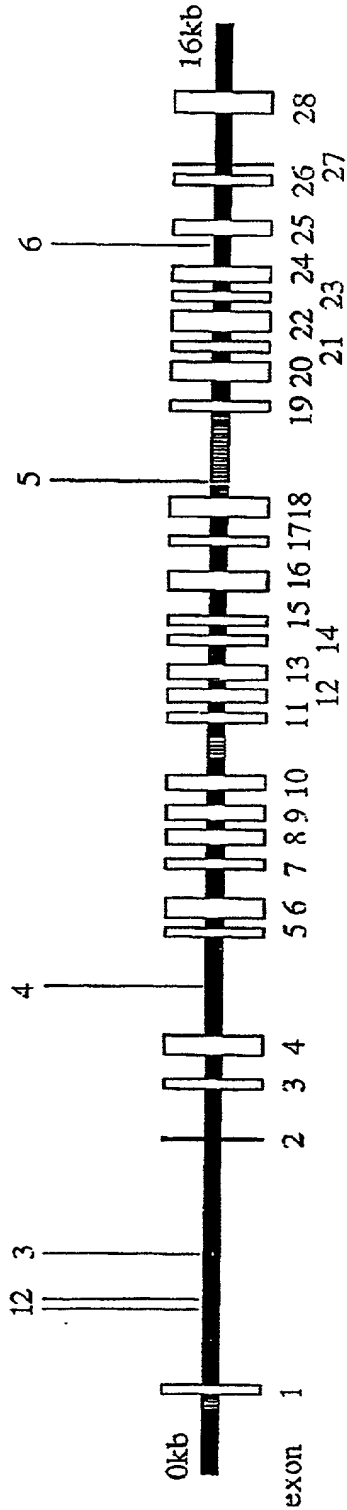


FIGURE 47

*arylalkylamine N-acetyltransferase(AANAT)*

Accession No. U40391

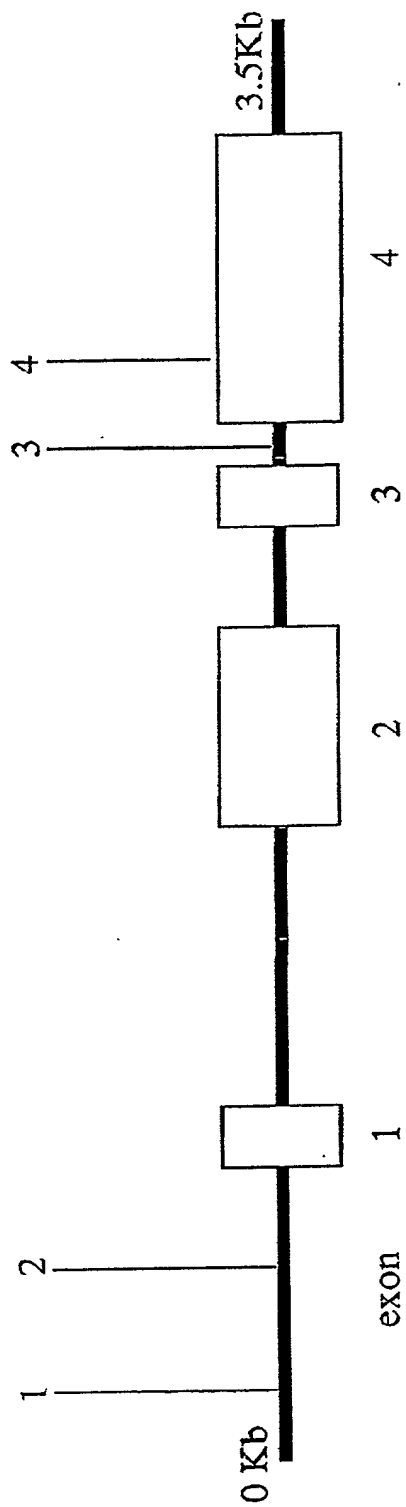


FIGURE 48



*N*-acetyltransferase, homolog of *S. cerevisiae* (*ARD1*)

Accession No. U52112

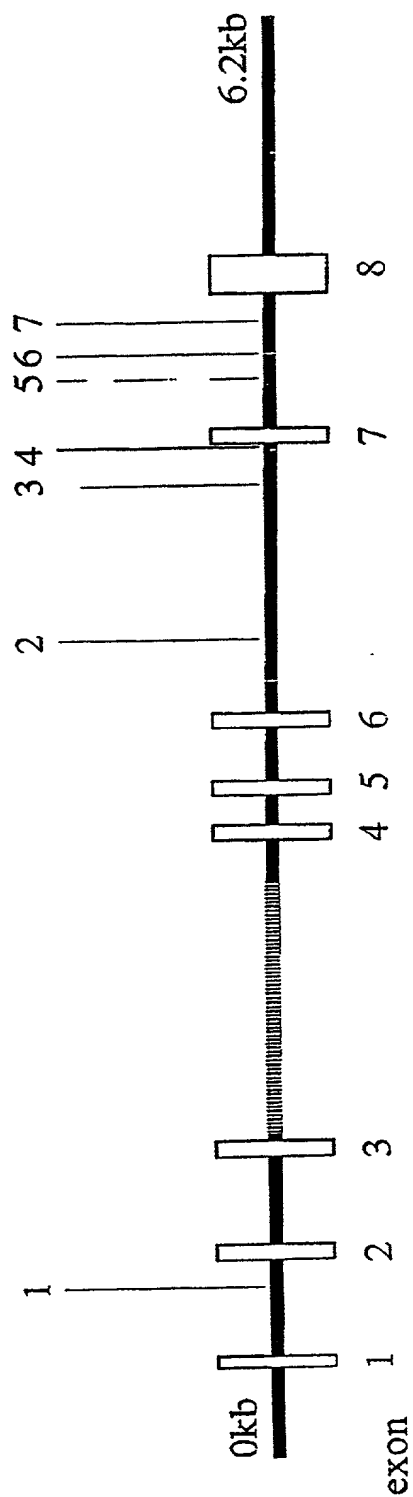


FIGURE 49

*N*-acetyltransferase (NAT1)

Accession No. X17059

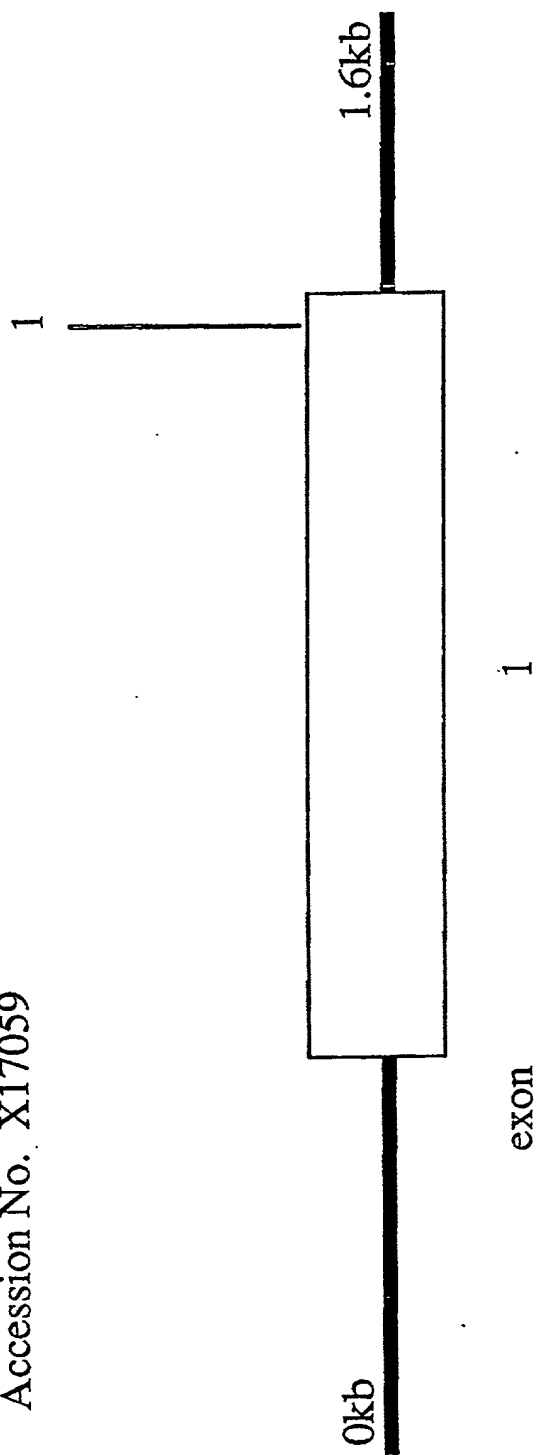


FIGURE 50

*arylamine N-acetyltransferase (NAT2)* Accession No.: I22255, AC025062, AC025648, D10870

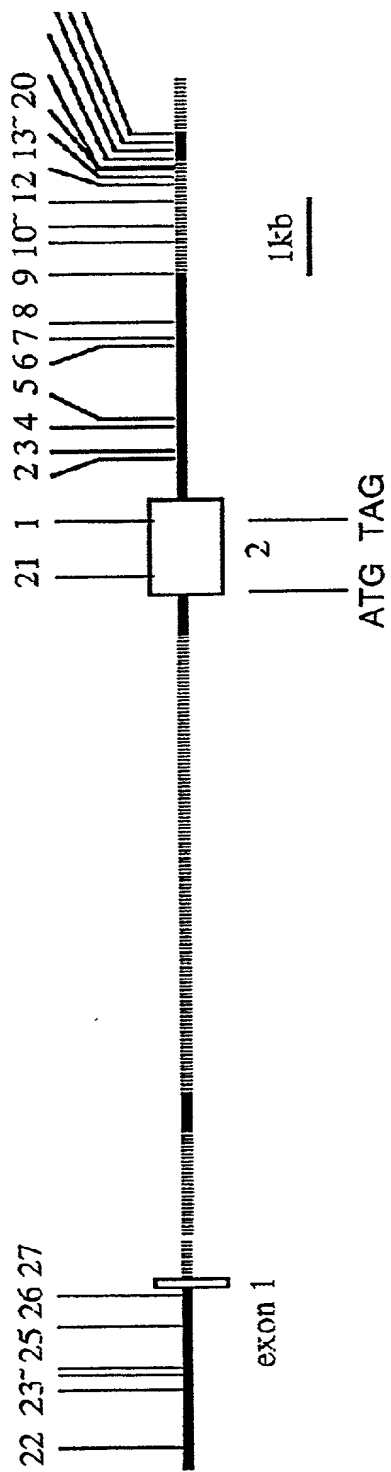


FIGURE 51

*Granzyme A (GZMA)*

Accession No. AC025790

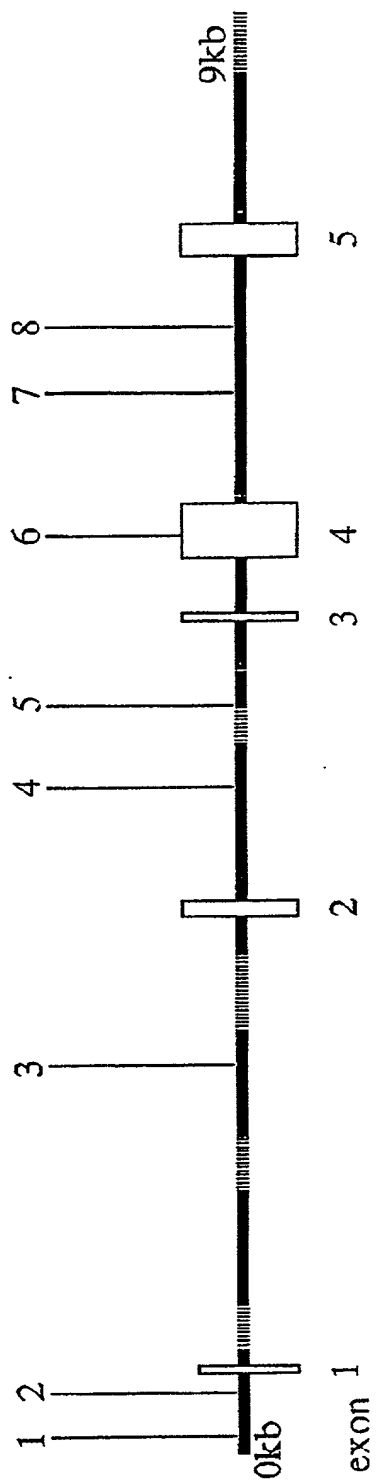


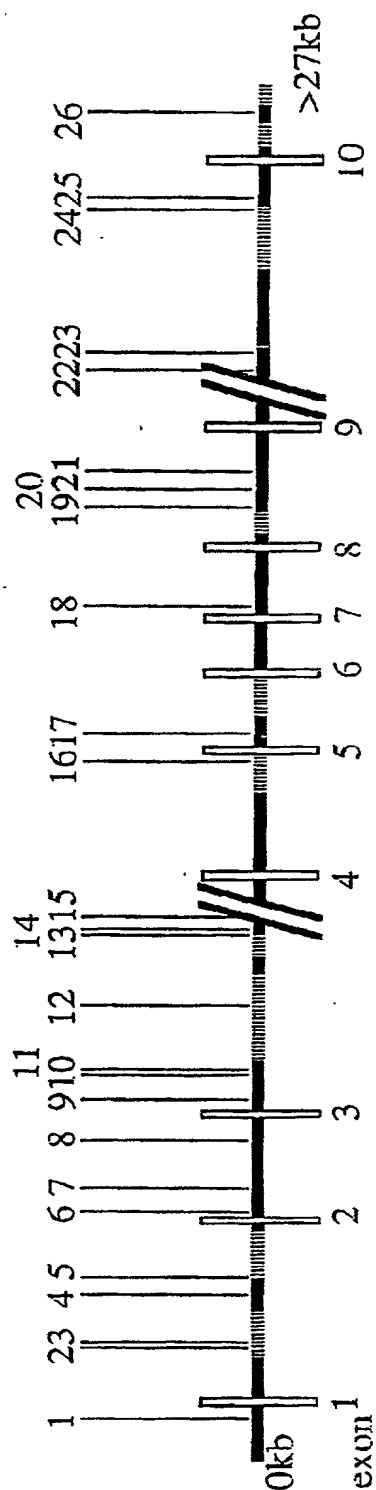
FIGURE 52



esterase D/formylglutathione hydrolase (ESD)

Accession No. AC136958

FIGURE 54



*dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)*

Accession No. D89060

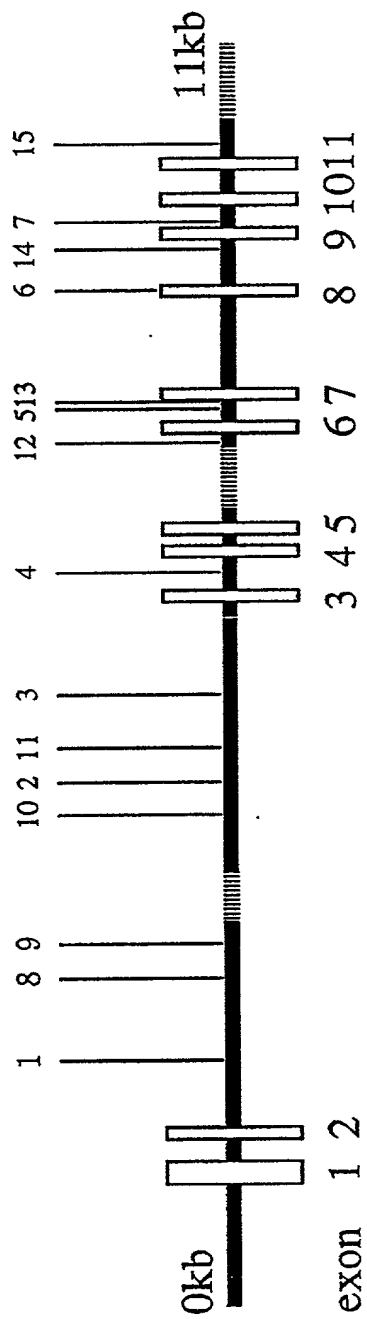


FIGURE 55

FIGURE 56

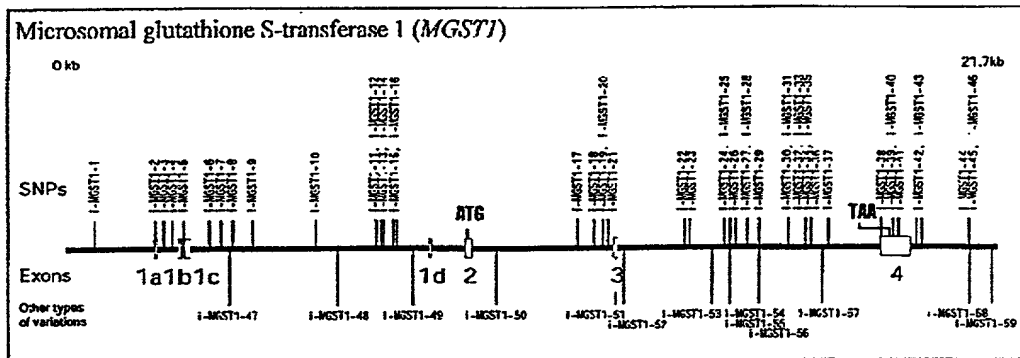


FIGURE 57

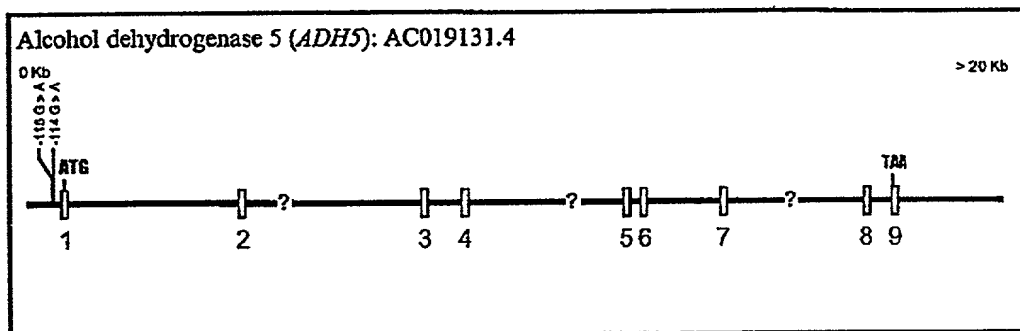


FIGURE 58

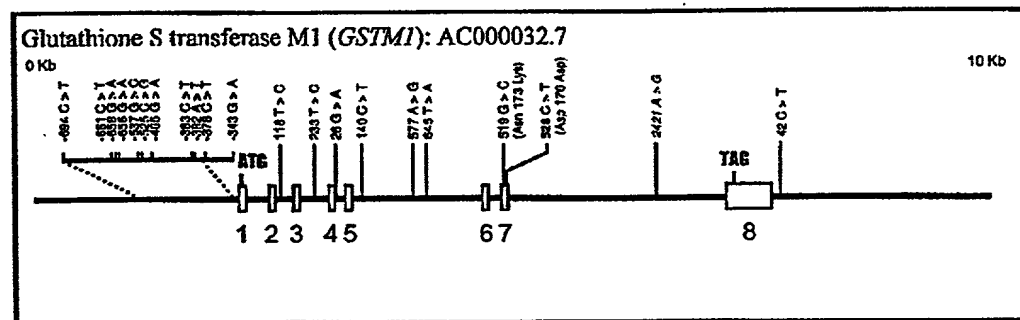


FIGURE 59

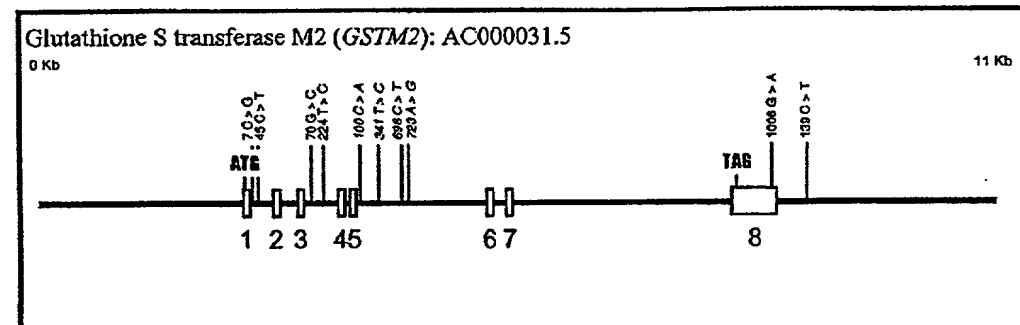




FIGURE 60

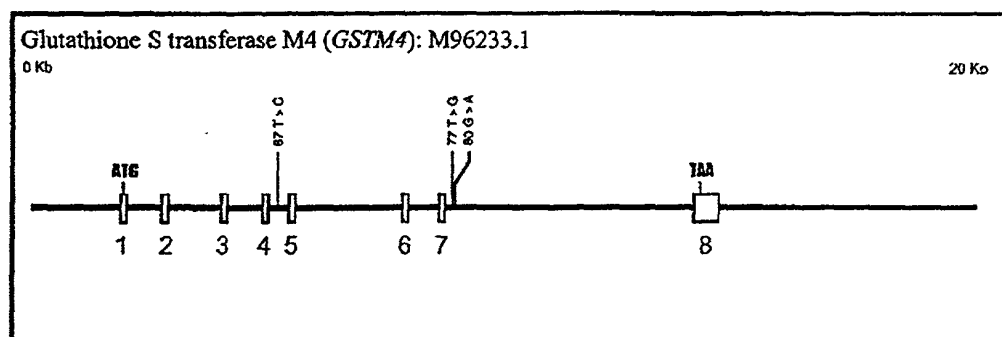


FIGURE 61

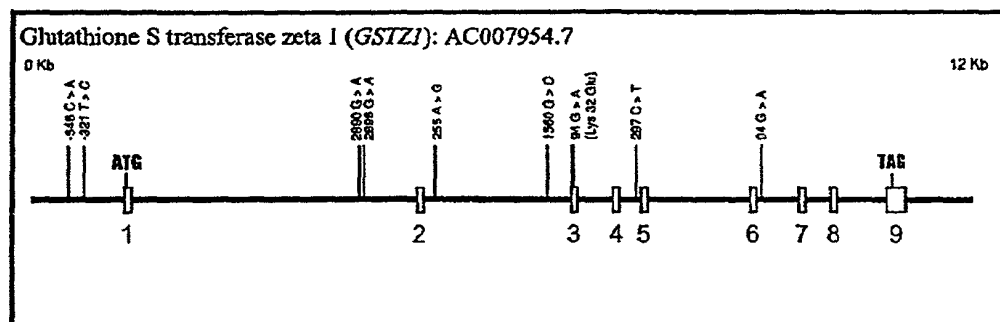


FIGURE 62

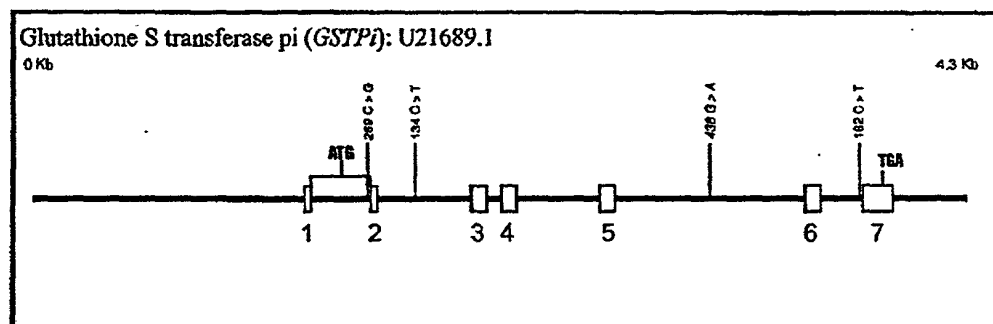
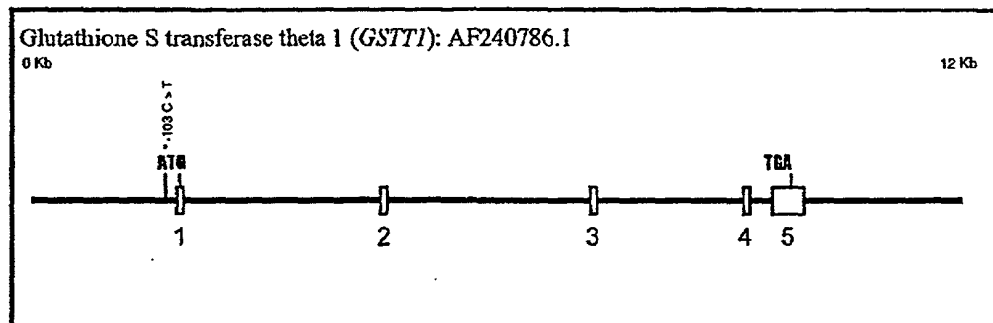


FIGURE 63



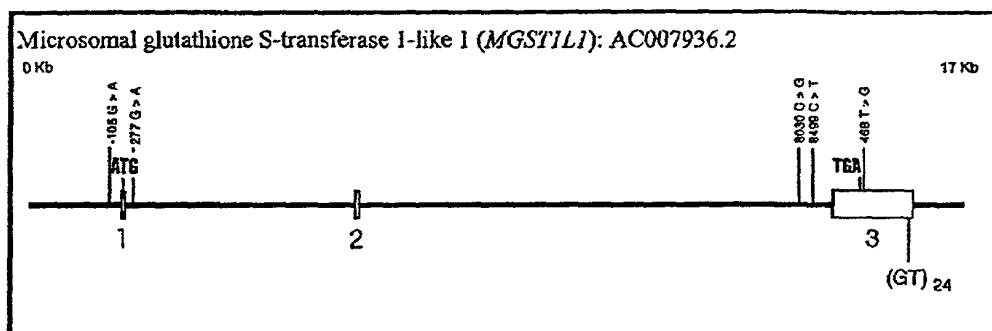
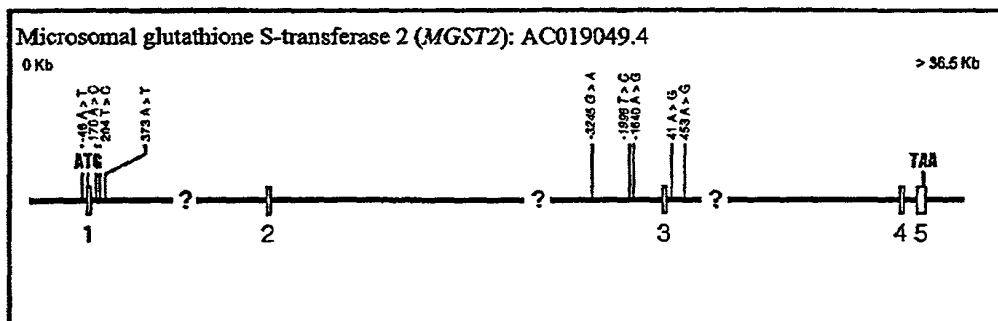
[illegible]

FIGURE 65



**FIGURE 66**

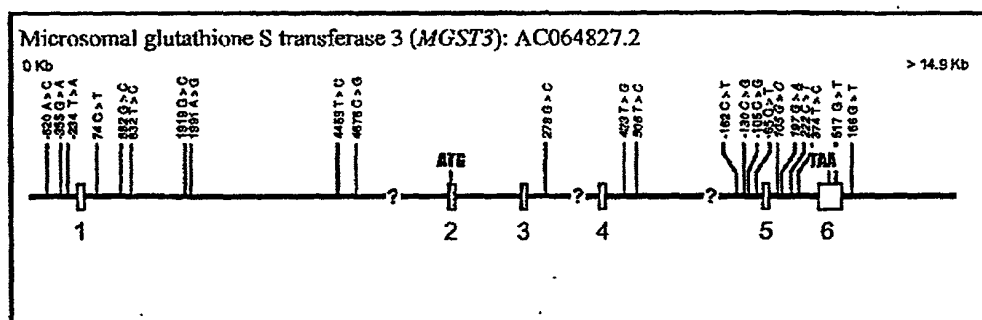


FIGURE 67

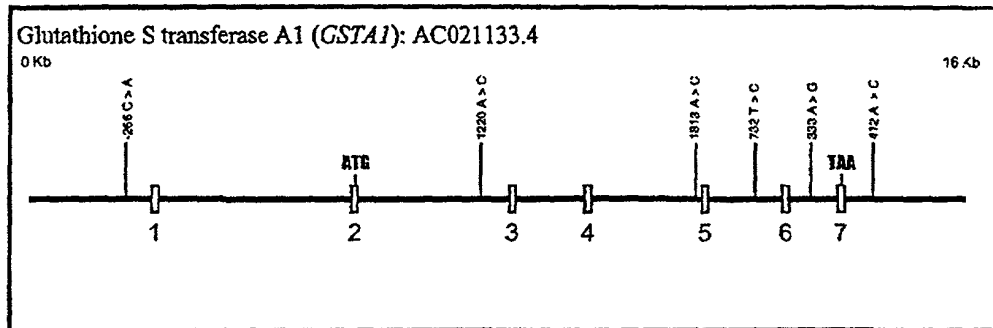


FIGURE 68

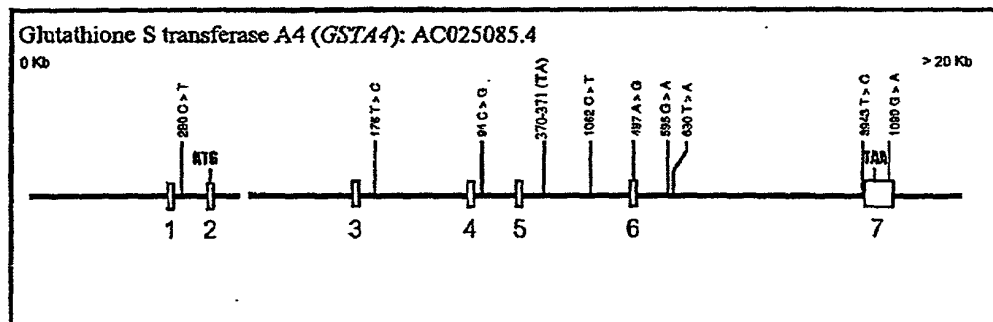


FIGURE 69

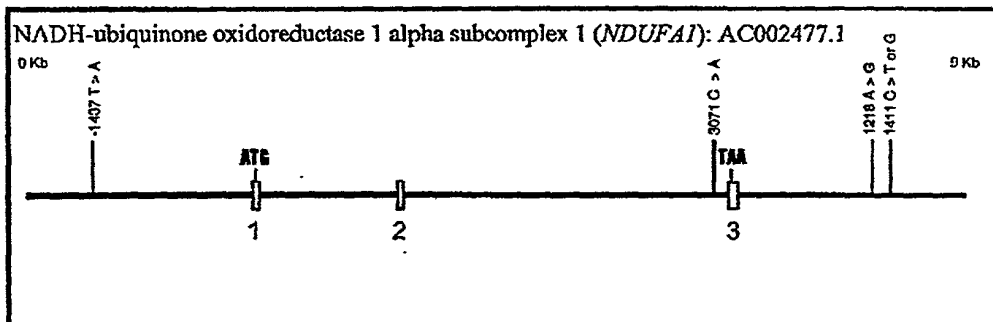


FIGURE 70

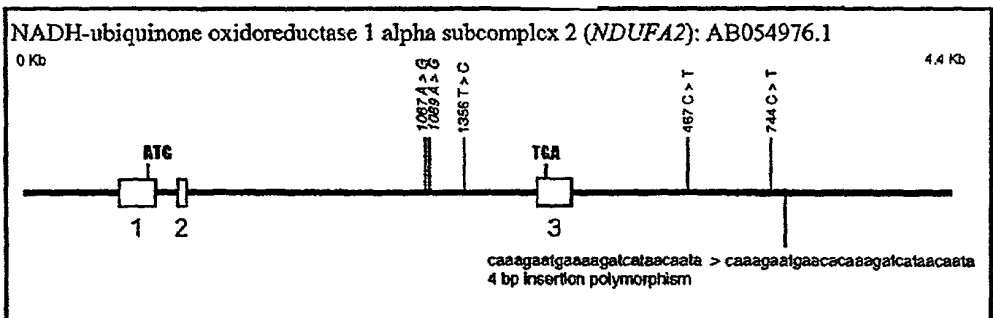


FIGURE 71

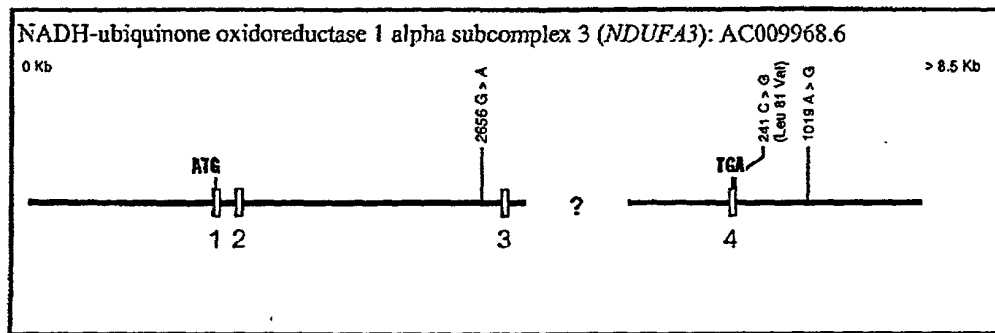


FIGURE 72

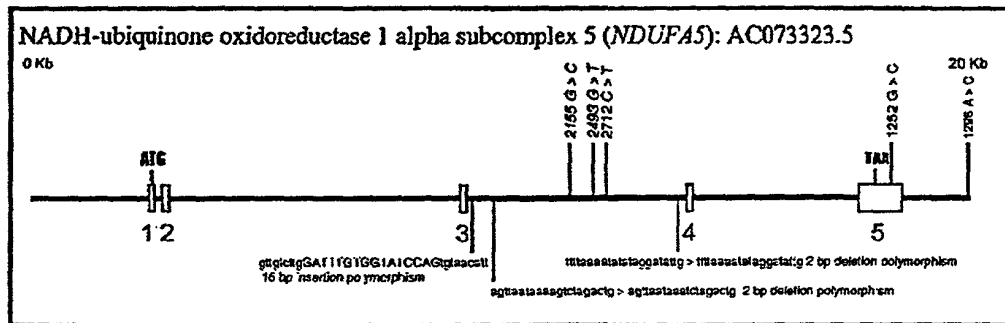


FIGURE 73

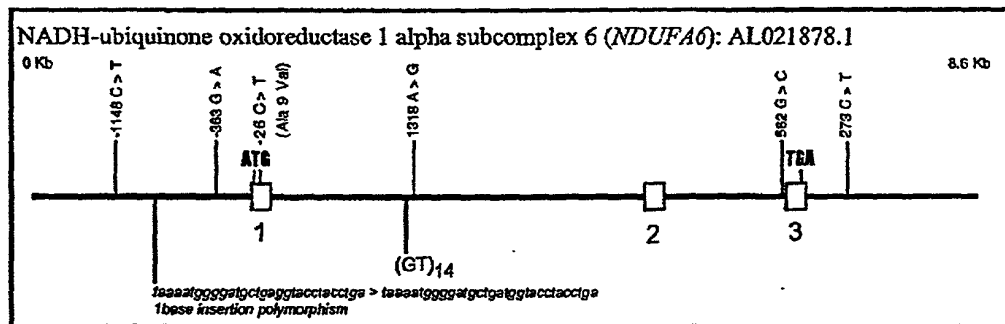
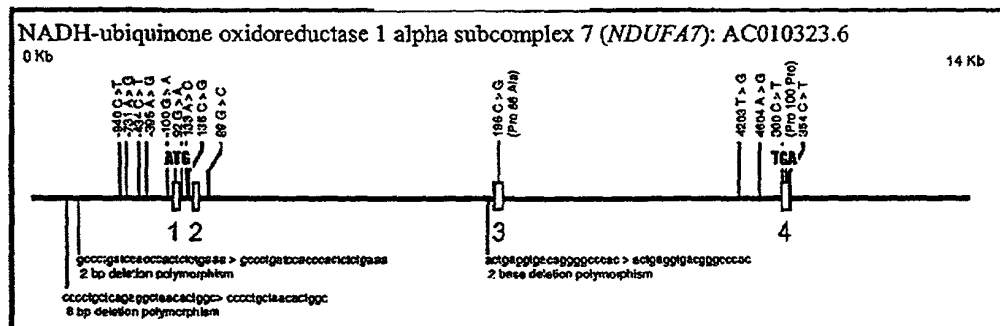
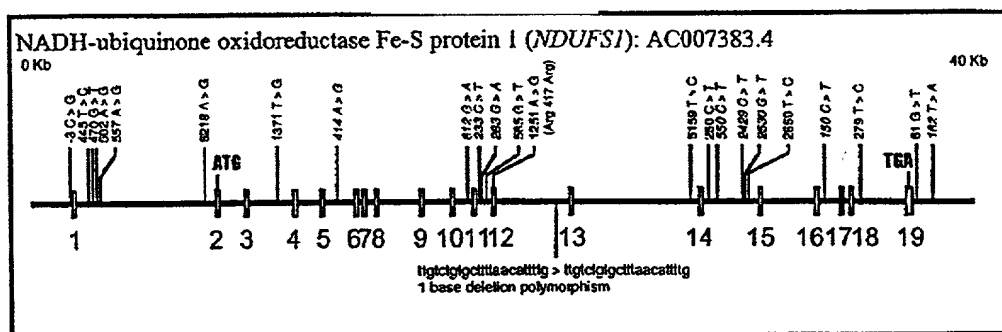


FIGURE 74



	1994	1995
1. Total population	100.0	100.0
2. Male	50.0	50.0
3. Female	50.0	50.0
4. Under 15	15.0	15.0
5. 15-64	65.0	65.0
6. 65+	20.0	20.0
7. Single	30.0	30.0
8. Married	50.0	50.0
9. Divorced	10.0	10.0
10. Widowed	10.0	10.0
11. Never married	10.0	10.0
12. Married, never divorced	40.0	40.0
13. Divorced, remarried	10.0	10.0
14. Widowed, remarried	10.0	10.0
15. Single, never married	10.0	10.0
16. Married, never divorced	40.0	40.0
17. Divorced, remarried	10.0	10.0
18. Widowed, remarried	10.0	10.0
19. Single, never married	10.0	10.0
20. Married, never divorced	40.0	40.0
21. Divorced, remarried	10.0	10.0
22. Widowed, remarried	10.0	10.0
23. Single, never married	10.0	10.0
24. Married, never divorced	40.0	40.0
25. Divorced, remarried	10.0	10.0
26. Widowed, remarried	10.0	10.0
27. Single, never married	10.0	10.0
28. Married, never divorced	40.0	40.0
29. Divorced, remarried	10.0	10.0
30. Widowed, remarried	10.0	10.0
31. Single, never married	10.0	10.0
32. Married, never divorced	40.0	40.0
33. Divorced, remarried	10.0	10.0
34. Widowed, remarried	10.0	10.0
35. Single, never married	10.0	10.0
36. Married, never divorced	40.0	40.0
37. Divorced, remarried	10.0	10.0
38. Widowed, remarried	10.0	10.0
39. Single, never married	10.0	10.0
40. Married, never divorced	40.0	40.0
41. Divorced, remarried	10.0	10.0
42. Widowed, remarried	10.0	10.0
43. Single, never married	10.0	10.0
44. Married, never divorced	40.0	40.0
45. Divorced, remarried	10.0	10.0
46. Widowed, remarried	10.0	10.0
47. Single, never married	10.0	10.0
48. Married, never divorced	40.0	40.0
49. Divorced, remarried	10.0	10.0
50. Widowed, remarried	10.0	10.0
51. Single, never married	10.0	10.0
52. Married, never divorced	40.0	40.0
53. Divorced, remarried	10.0	10.0
54. Widowed, remarried	10.0	10.0
55. Single, never married	10.0	10.0
56. Married, never divorced	40.0	40.0
57. Divorced, remarried	10.0	10.0
58. Widowed, remarried	10.0	10.0
59. Single, never married	10.0	10.0
60. Married, never divorced	40.0	40.0
61. Divorced, remarried	10.0	10.0
62. Widowed, remarried	10.0	10.0
63. Single, never married	10.0	10.0
64. Married, never divorced	40.0	40.0
65. Divorced, remarried	10.0	10.0
66. Widowed, remarried	10.0	10.0
67. Single, never married	10.0	10.0
68. Married, never divorced	40.0	40.0
69. Divorced, remarried	10.0	10.0
70. Widowed, remarried	10.0	10.0
71. Single, never married	10.0	10.0
72. Married, never divorced	40.0	40.0
73. Divorced, remarried	10.0	10.0
74. Widowed, remarried	10.0	10.0
75. Single, never married	10.0	10.0
76. Married, never divorced	40.0	40.0
77. Divorced, remarried	10.0	10.0
78. Widowed, remarried	10.0	10.0
79. Single, never married	10.0	10.0
80. Married, never divorced	40.0	40.0
81. Divorced, remarried	10.0	10.0
82. Widowed, remarried	10.0	10.0
83. Single, never married	10.0	10.0
84. Married, never divorced	40.0	40.0
85. Divorced, remarried	10.0	10.0
86. Widowed, remarried	10.0	10.0
87. Single, never married	10.0	10.0
88. Married, never divorced	40.0	40.0
89. Divorced, remarried	10.0	10.0
90. Widowed, remarried	10.0	10.0
91. Single, never married	10.0	10.0
92. Married, never divorced	40.0	40.0
93. Divorced, remarried	10.0	10.0
94. Widowed, remarried	10.0	10.0
95. Single, never married	10.0	10.0
96. Married, never divorced	40.0	40.0
97. Divorced, remarried	10.0	10.0
98. Widowed, remarried	10.0	10.0
99. Single, never married	10.0	10.0
100. Married, never divorced	40.0	40.0
101. Divorced, remarried	10.0	10.0
102. Widowed, remarried	10.0	10.0
103. Single, never married	10.0	10.0
104. Married, never divorced	40.0	40.0
105. Divorced, remarried	10.0	10.0
106. Widowed, remarried	10.0	10.0
107. Single, never married	10.0	10.0
108. Married, never divorced	40.0	40.0
109. Divorced, remarried	10.0	10.0
110. Widowed, remarried	10.0	10.0
111. Single, never married	10.0	10.0



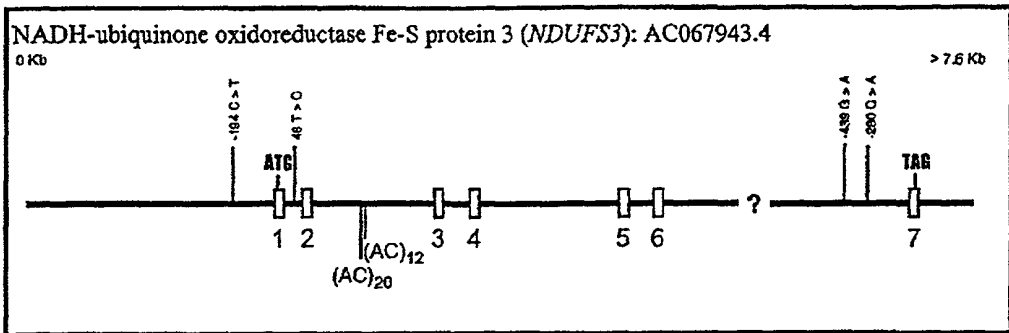
[illegible]

FIGURE 80

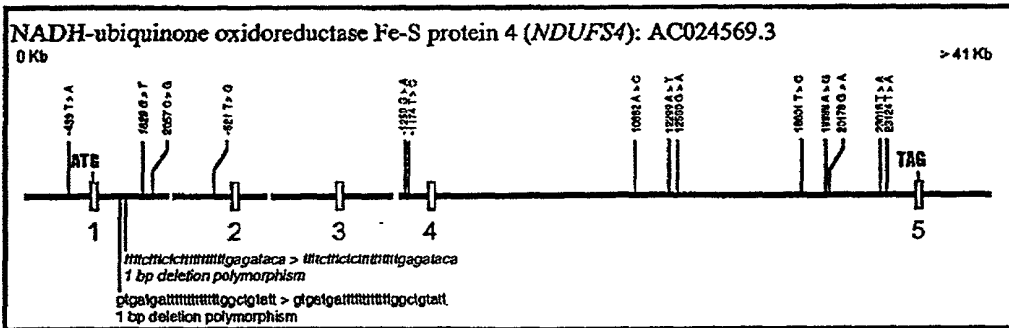


FIGURE 81

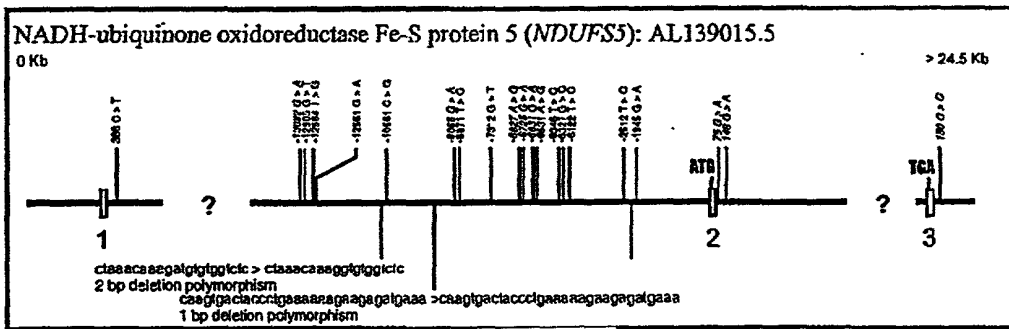
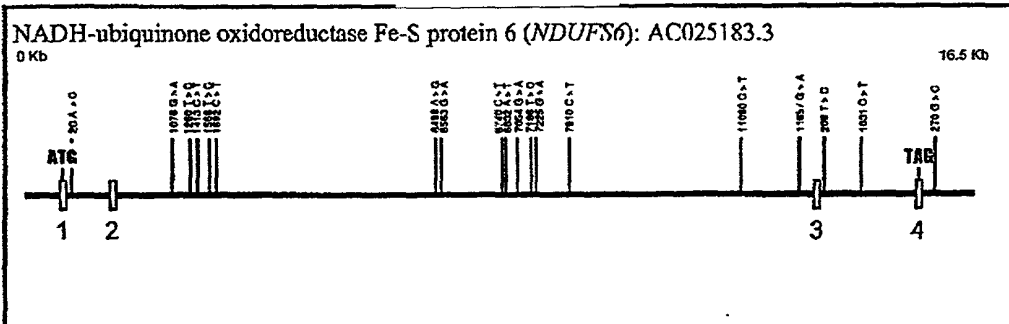


FIGURE 82



FOR THE "CELL" DATABASE

# SNP Information for IMS-JST104917

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST104917  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	806730	12	4625643

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104917](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104917)

12/17/2001

**ABCA1**      **ACCESSION**      **AF275948.1**



*Catechol-O-methyltransferase (COMT)*

ACCESSION AC000080

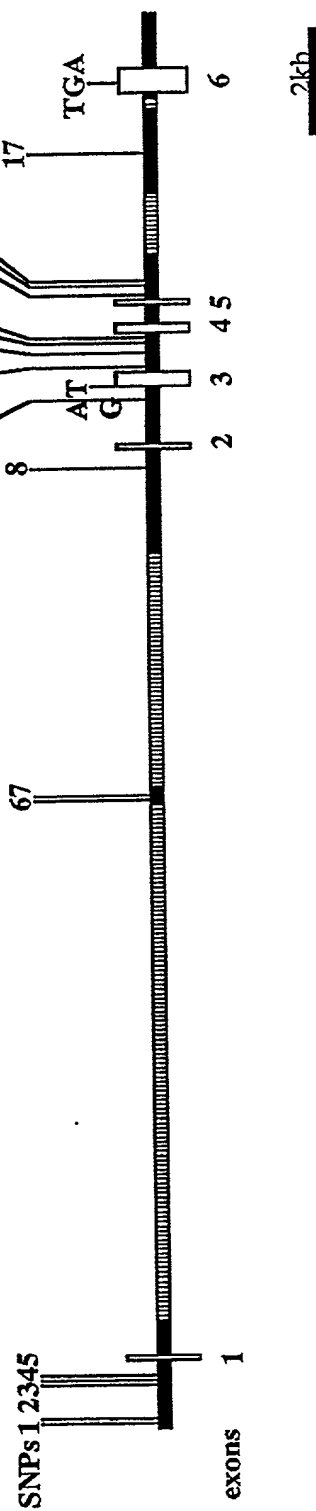
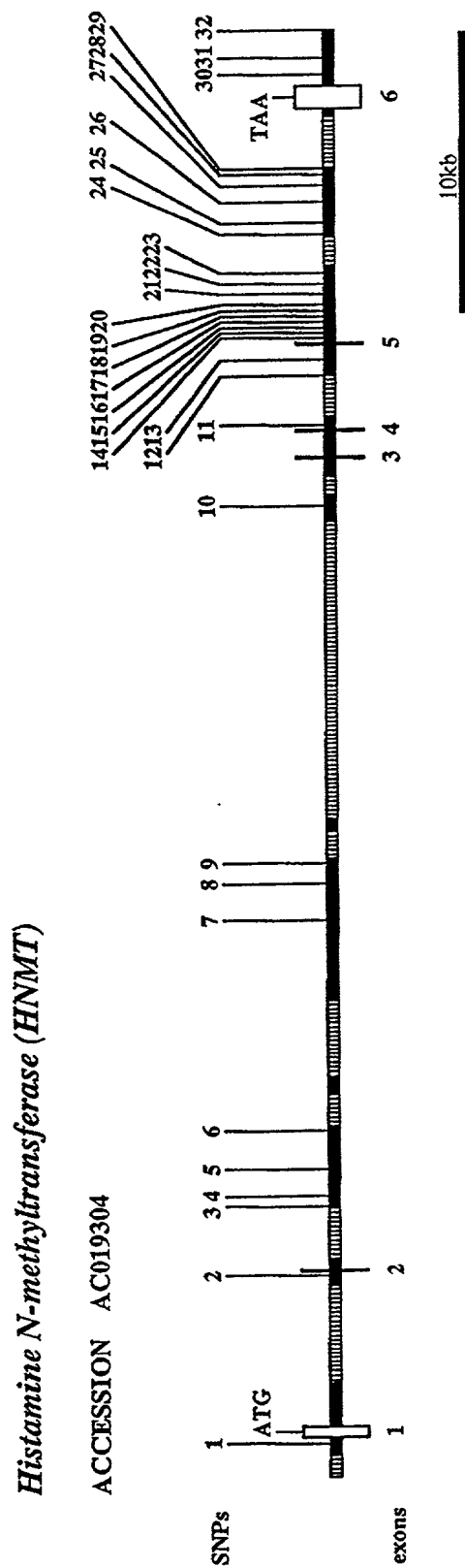


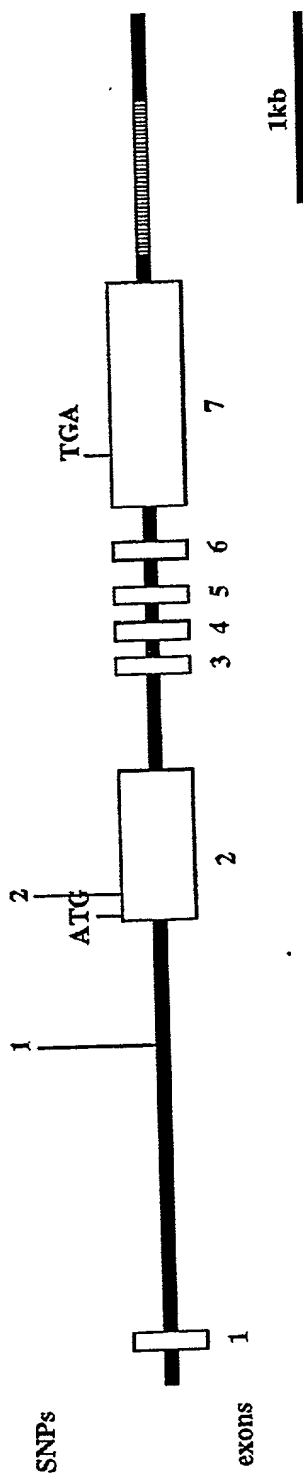
FIGURE 88

FIGURE 89



## Cytochrome P450, subfamily I, polypeptide 1 (CYP1A1)

**ACCESSION X04300**



*Cytochrome P450, subfamily 1, polypeptide 2 (CYP1A2)*

ACCESSION AC020705

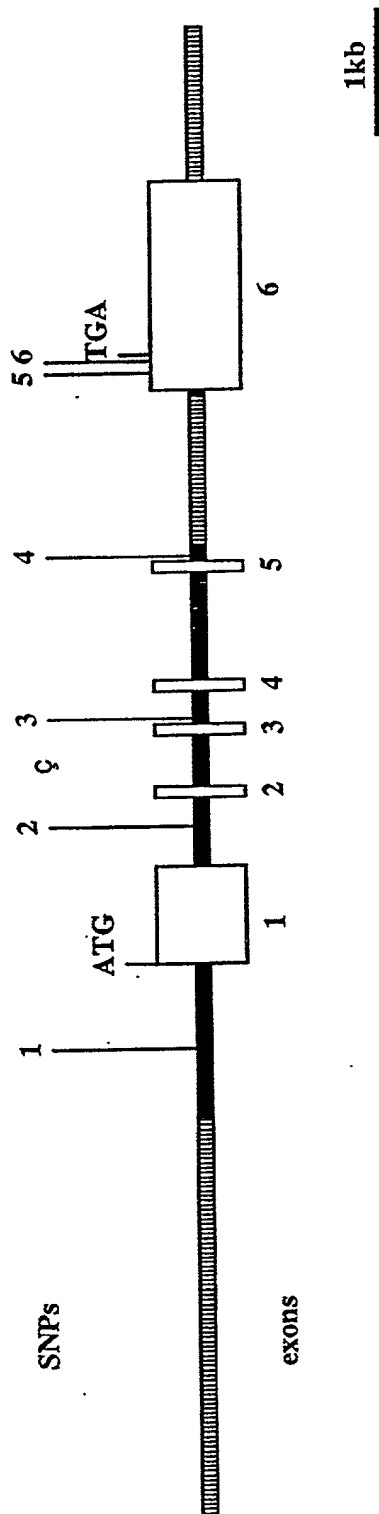


FIGURE 91



*Arylacetamide deacetylase (AADAC)*

ACCESSION AC068647

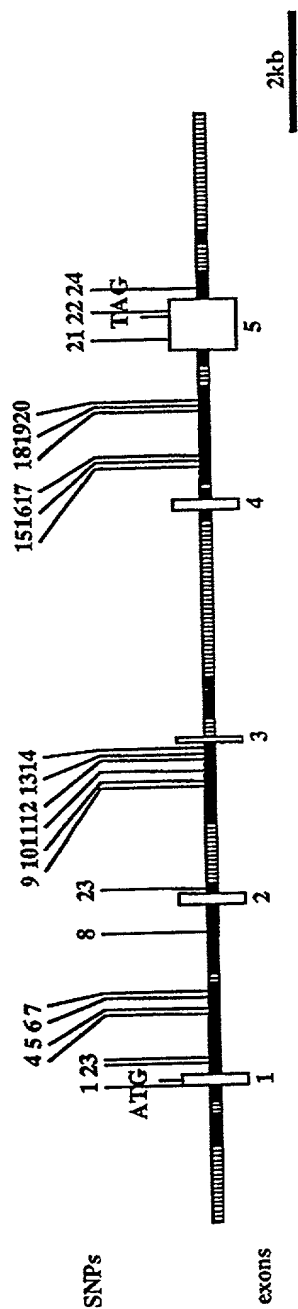


FIGURE 93

FIGURE 94

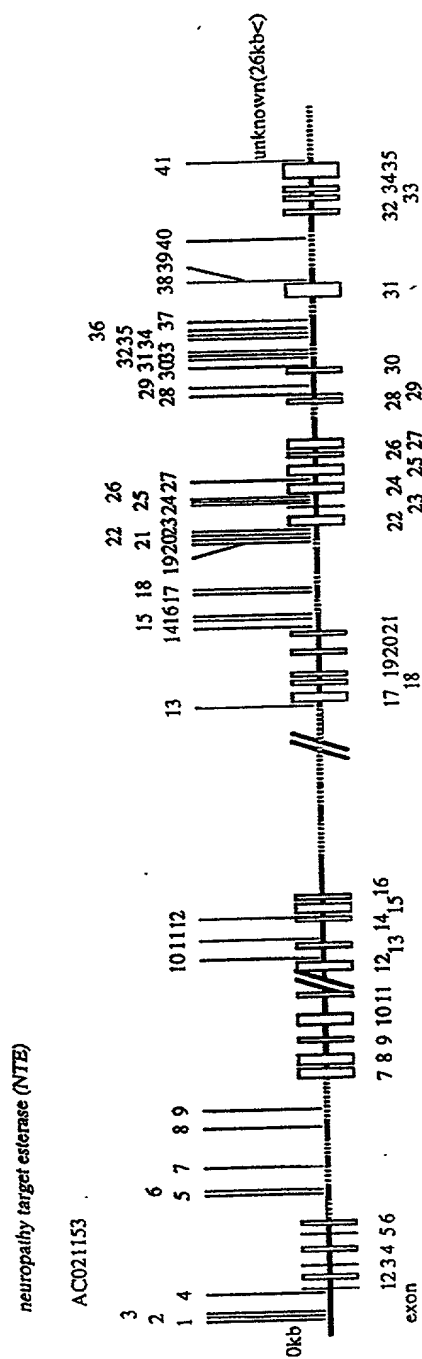
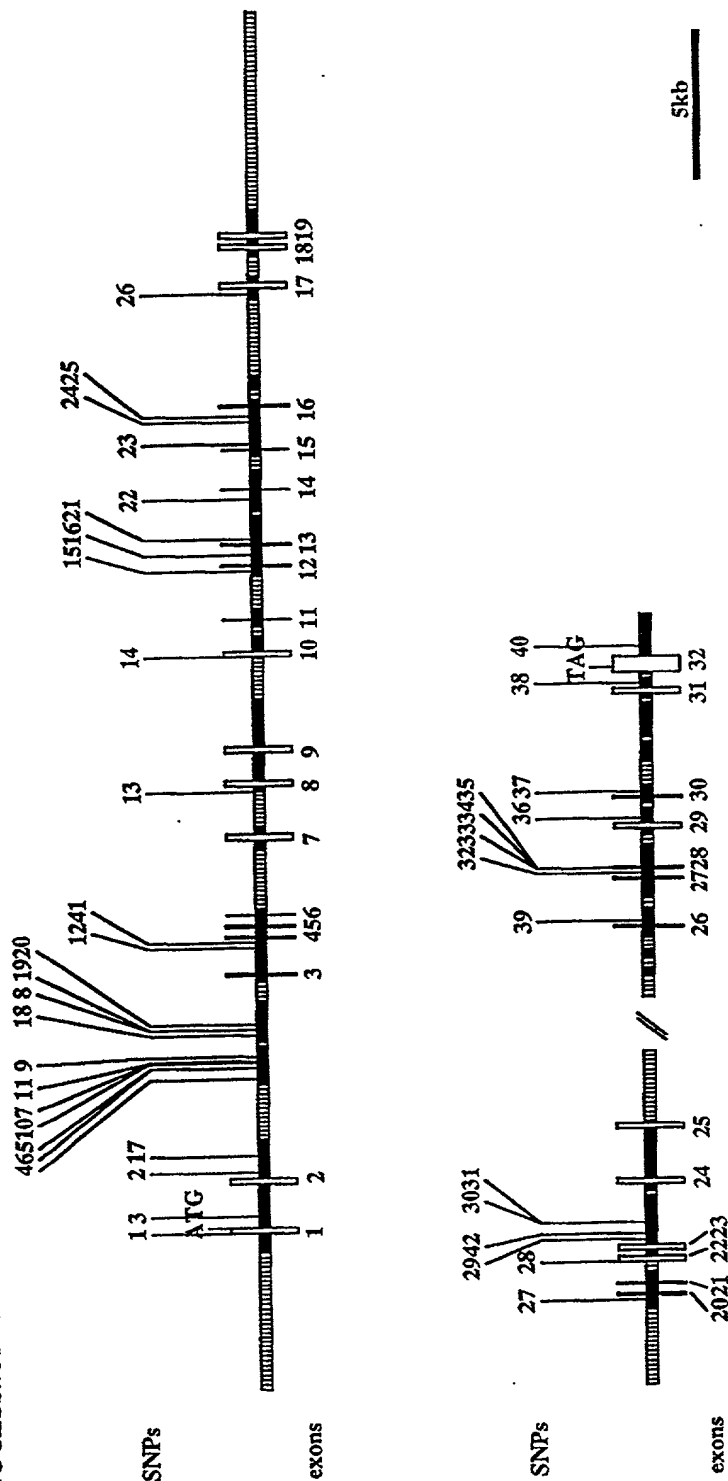


FIGURE 95

ATP-binding cassette, sub-family C (CFTR/MRP), member2 (MRP2)

ACCESSION AL392107





# Sequence

Observed : C/T  
 3' Assay : CTCCTAGTT GCGGGAGTA GCGGGAAGAG CCTTCCTCGC GTTAATTATG CAATAAGAAAG  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_022171.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map :  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 526155 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_022171.2 20010209\_1  
 Amplified region : 525548..526488 in NT\_022171  
 size : 941

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TTTTCCTGGAT GGAGGCCAG C	

FIGURE 97

*ATP-binding cassette, sub-family B, member 3 (ABCB3)*  
ACCESSION X66401

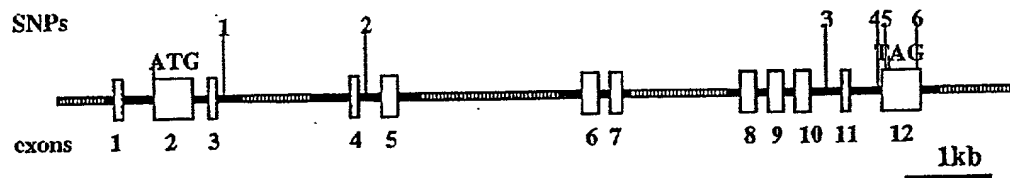


FIGURE 98

*ATP-binding cassette, sub-family B, member 7 (ABCB7)*  
ACCESSION AL360179

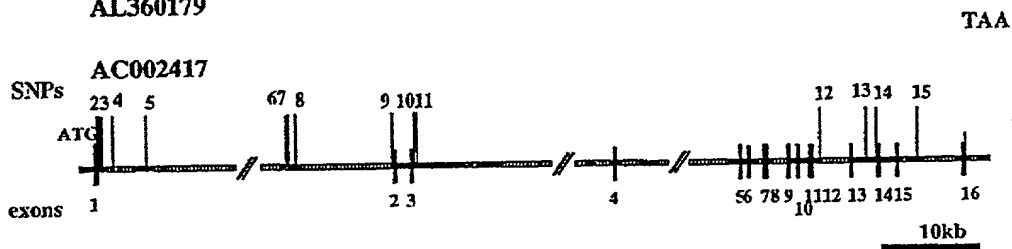
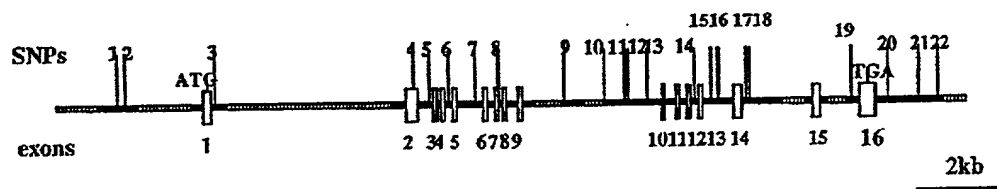


FIGURE 99

*ATP-binding cassette, sub-family B, member 8 (ABCB8)*  
ACCESSION AC010973



TTCTGCTTGGGAGGCGGATCA

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TGGGCGCGGT GGCTCAGCC TGTAATCCCA GCACTTGGG AGGCCGAGGT GGGCGGATCA  
Observed : T/C  
3' Assay : GAGTCAGGA GATCGAGACC ACGATGAAAC CCGTCTCTA CTAAATATAC AAAAAATTAG  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

### Screened Sequence

Accession No. : NT\_006124.3 ([Graphical View of this Entry](#))  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 468642 ([View SNP position in this record](#))

### Method

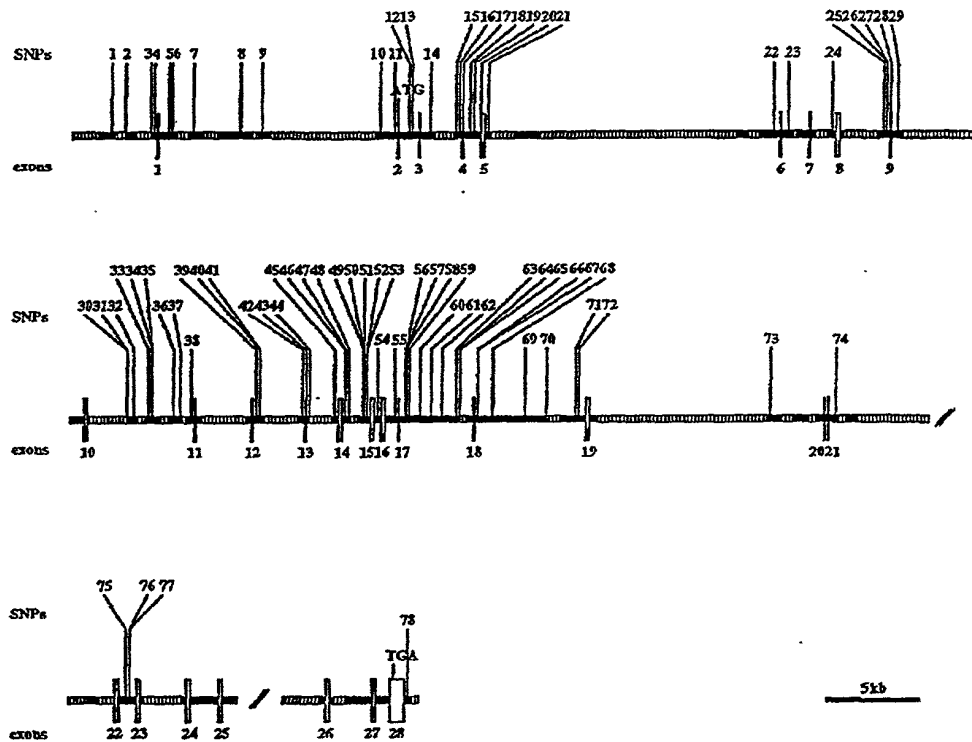
PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_006124.3 20010416\_6  
Amplified region : 467851..468999 in NT\_006124  
size : 1149  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

[illegible]

ACCESSION AC008177  
AC069137



**FIGURE 103**

**Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)**

ACCESSION AL356793

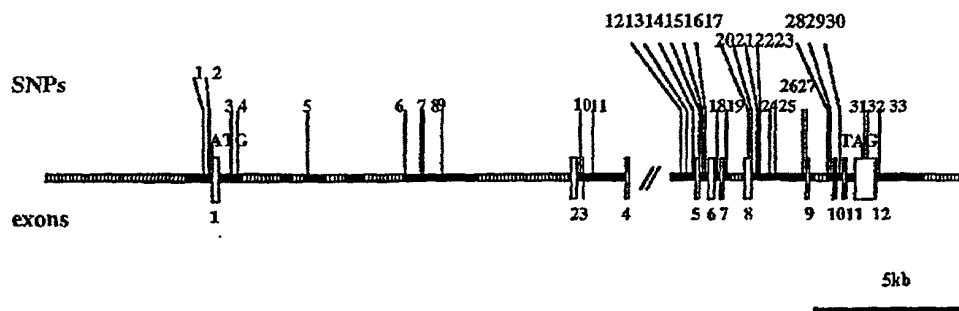


FIGURE 104

*Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)*

ACCESSION AC009974

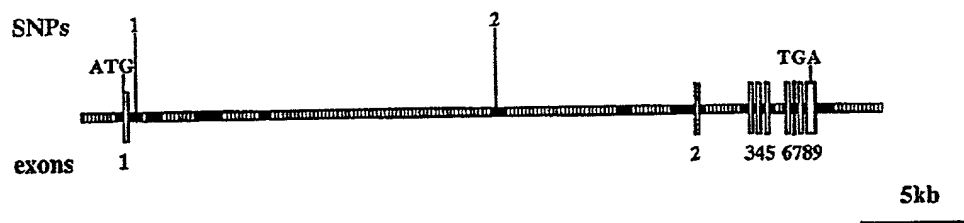


FIGURE 105

*Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2)*

ACCESSION AC005336

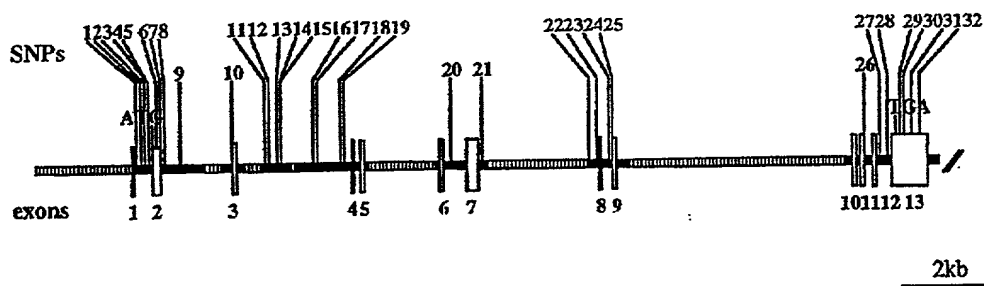


FIGURE 106

*Cytochrome P450, subfamily 4F, polypeptide 3 (CYP4F3)*

ACCESSION AD000685

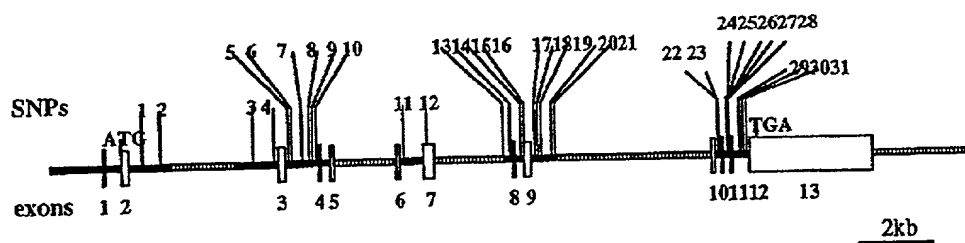


FIGURE 107

*Cytochrome P450, subfamily 4F, polypeptide 8 (CYP4F8)*

ACCESSION AC068845

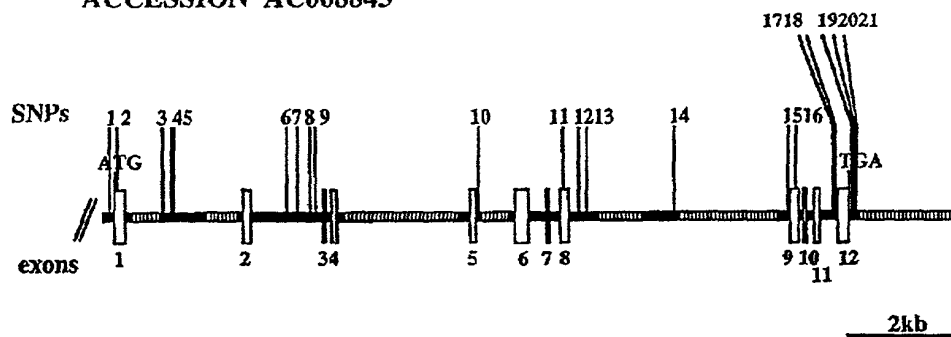


FIGURE 108

*Aldehyde dehydrogenase 1 (ALDH1)*

ACCESSION

AC009284

AL162416

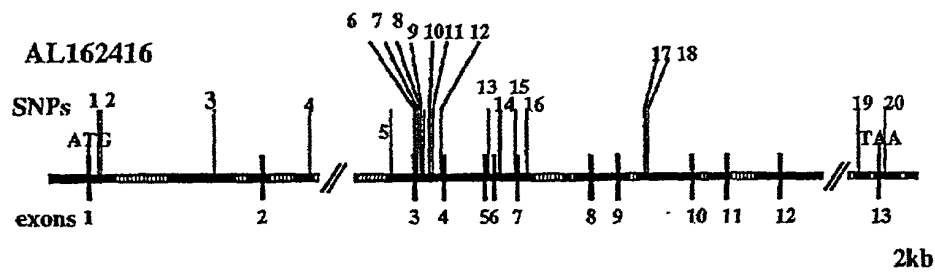


FIGURE 109

*Aldehyde dehydrogenase 2 (ALDH2)*

ACCESSION AC002996

AC003029

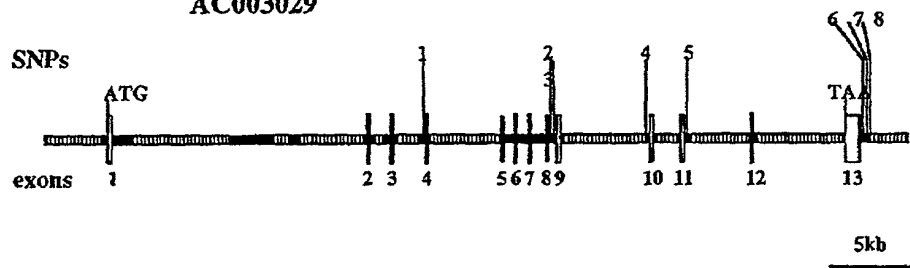


FIGURE 110

*Aldehyde dehydrogenase 7 (ALDH7)*

ACCESSION AC004923

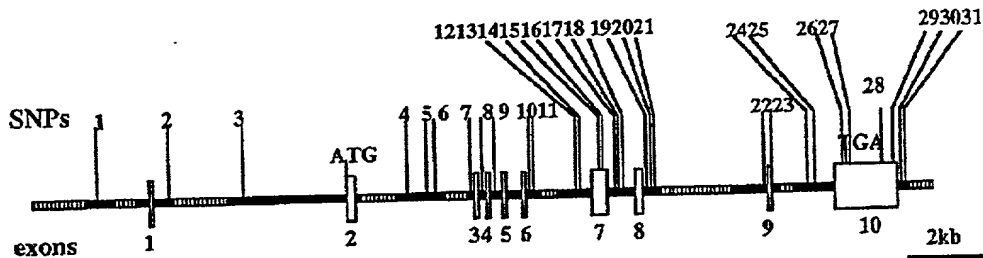


FIGURE 111

*Aldehyde dehydrogenase 8 (ALDH8)*

ACCESSION AC021987

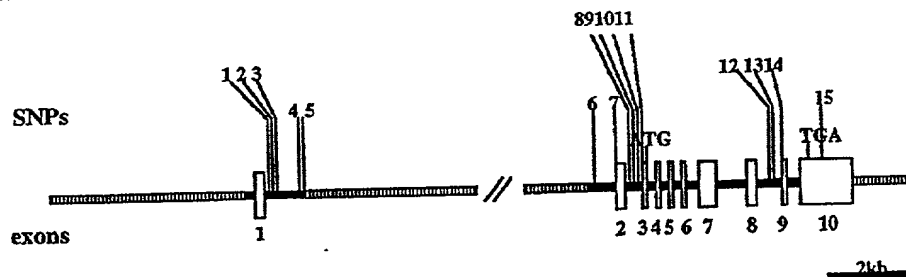


FIGURE 112

*Aldehyde dehydrogenase 9 (ALDH9)*

ACCESSION AL451074

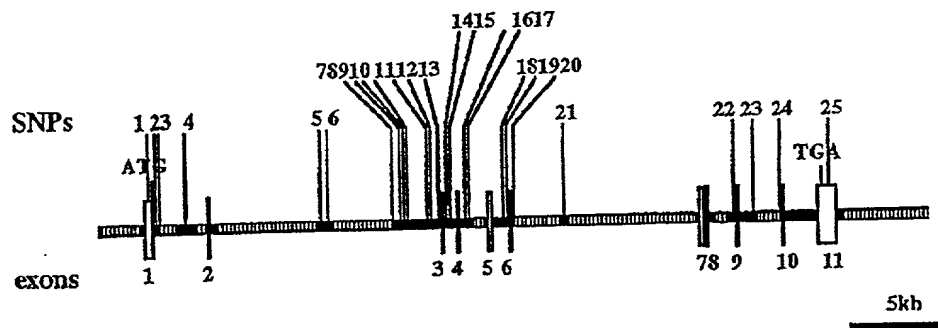


FIGURE 113

*Aldehyde dehydrogenase 10 (ALDH10)*

ACCESSION AC005722

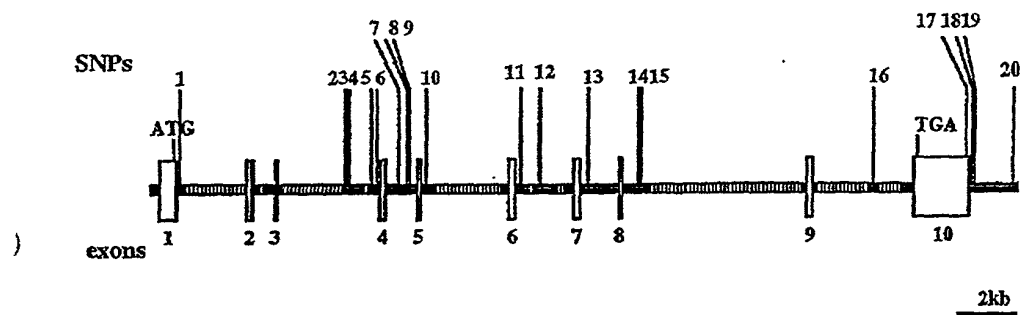




FIGURE 114

*ATP binding cassette, sub-family C, member 7 (ABCC7)*

ACCESSION AC000111  
AC000061

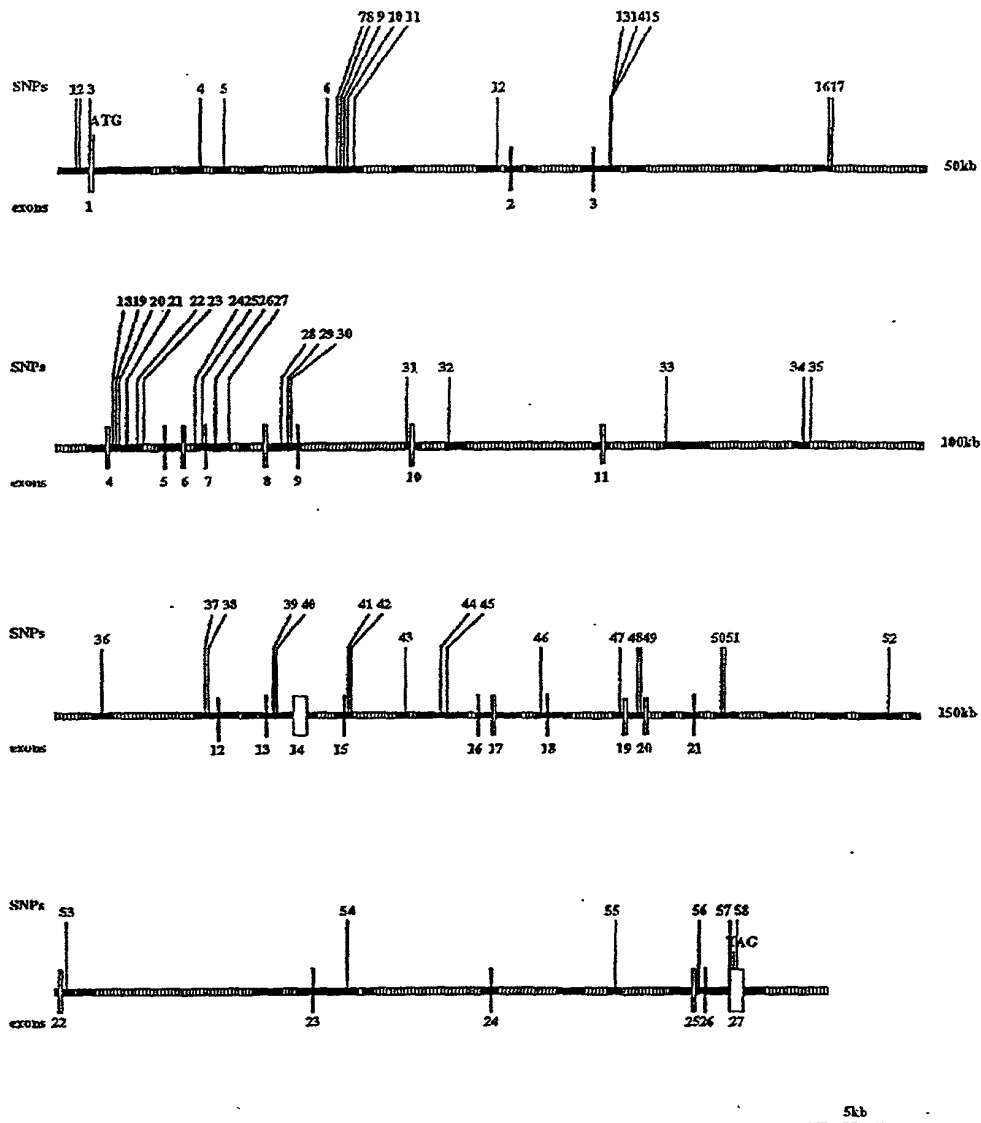


FIGURE 115

ATP binding cassette, sub-family C, member 8 (ABCC8)

ACCESSION AC000406

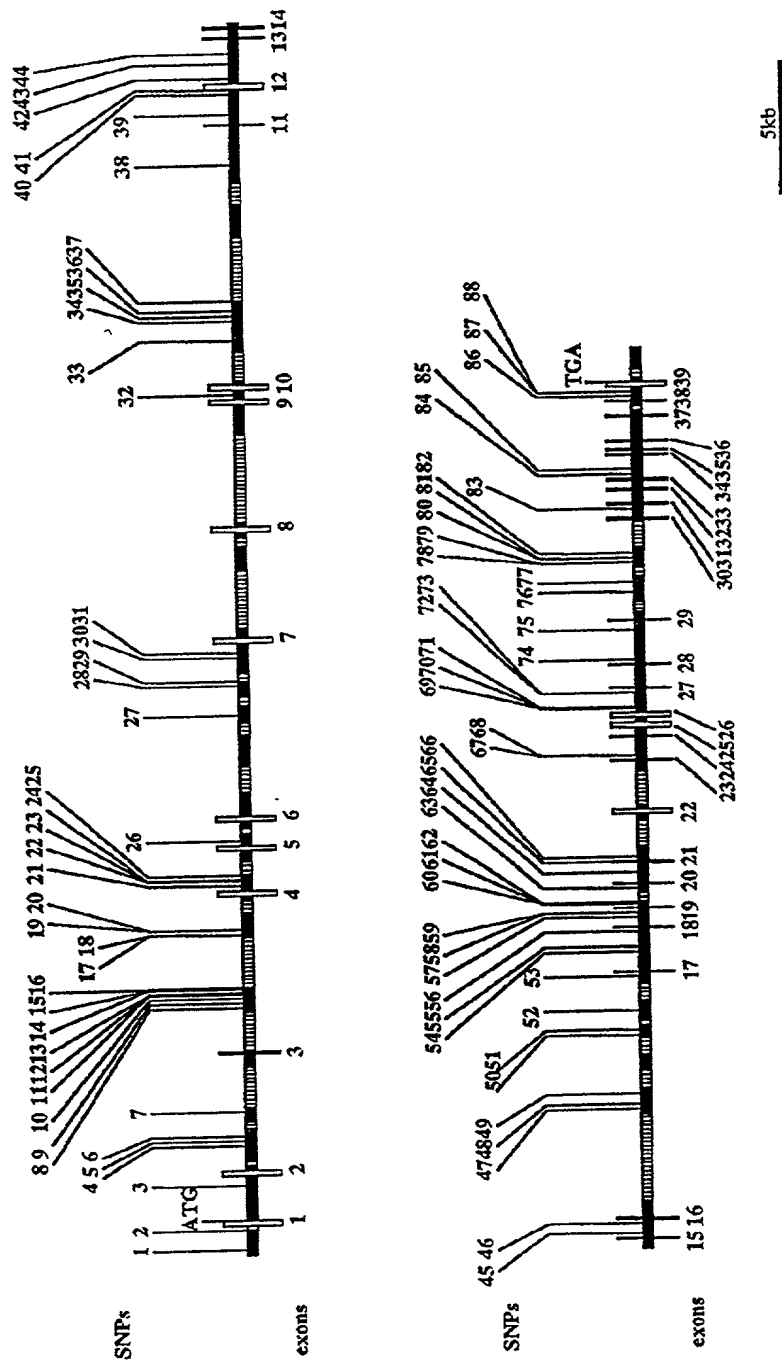
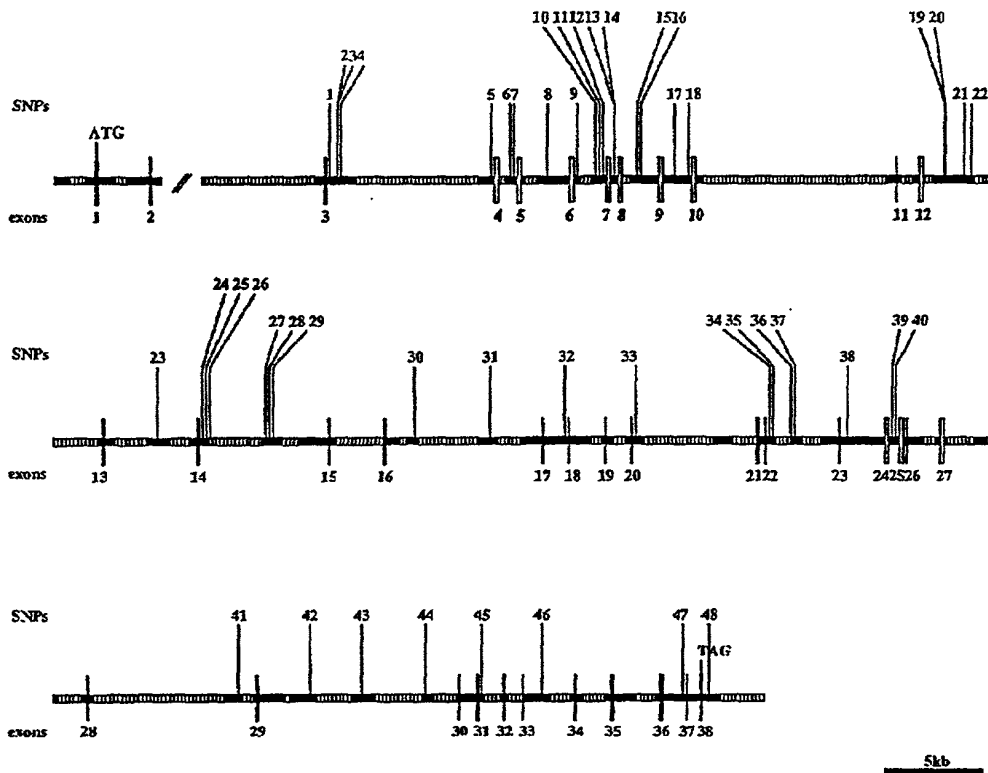


FIGURE 116

*ATP binding cassette, sub-family C, member 9 (ABCC9)*

ACCESSION AC084806  
AC008250



*Carboxylesterase 1 (CES1)*

ACCESSION AC007602

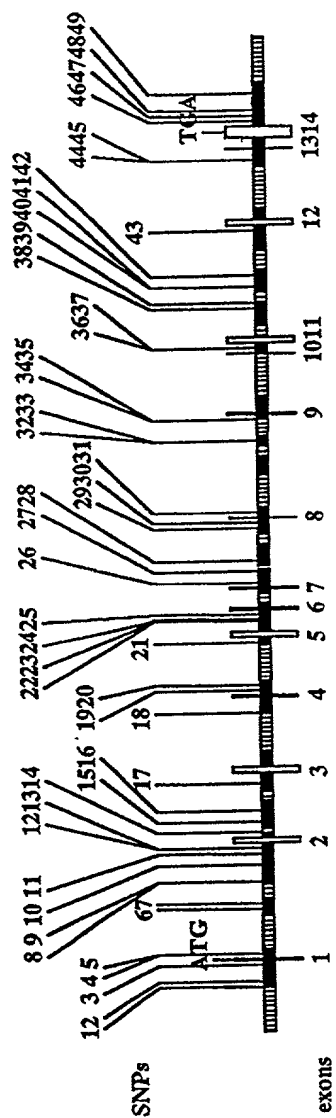
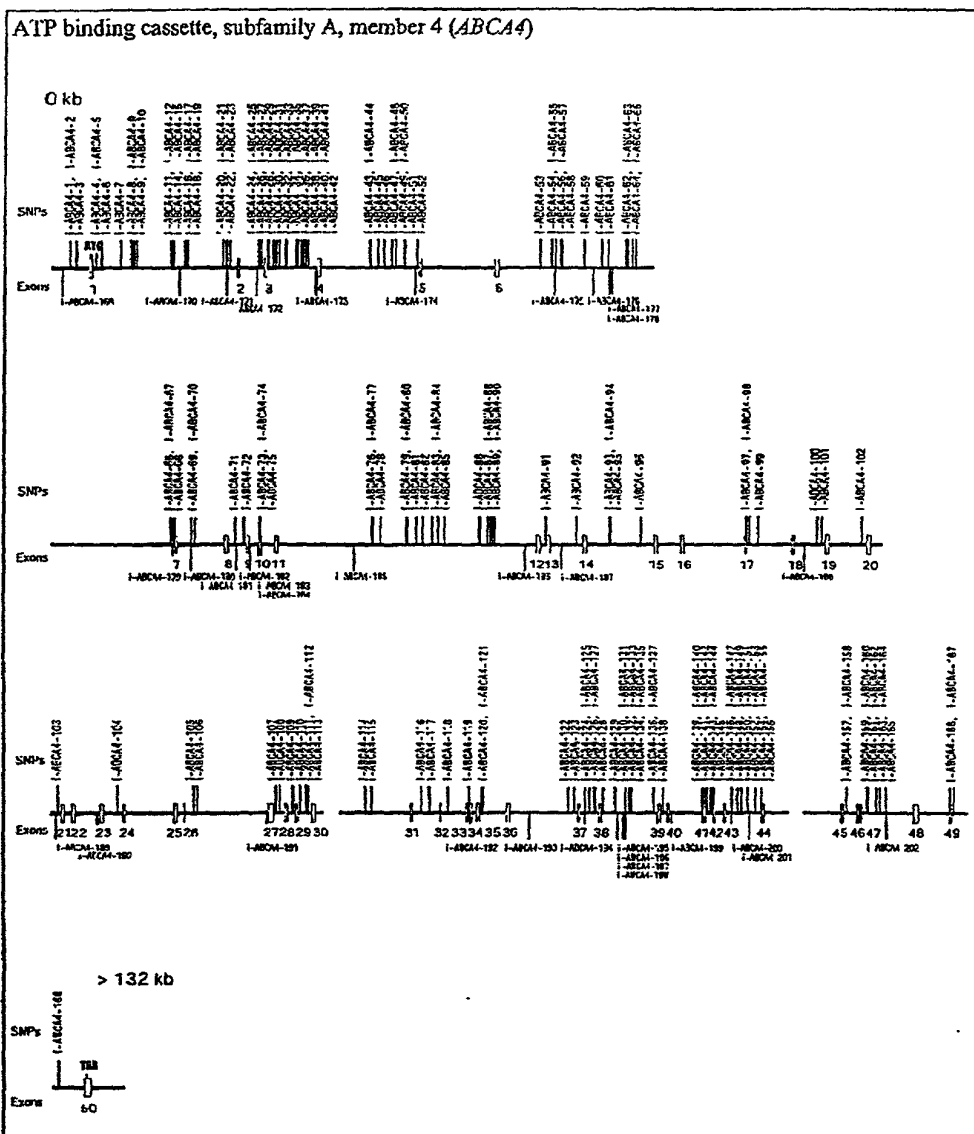
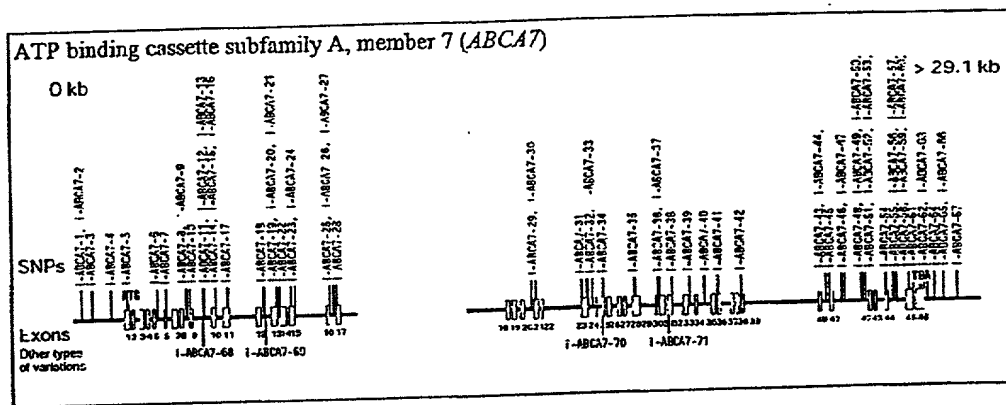


FIGURE 117

[illegible]

[illegible]

—

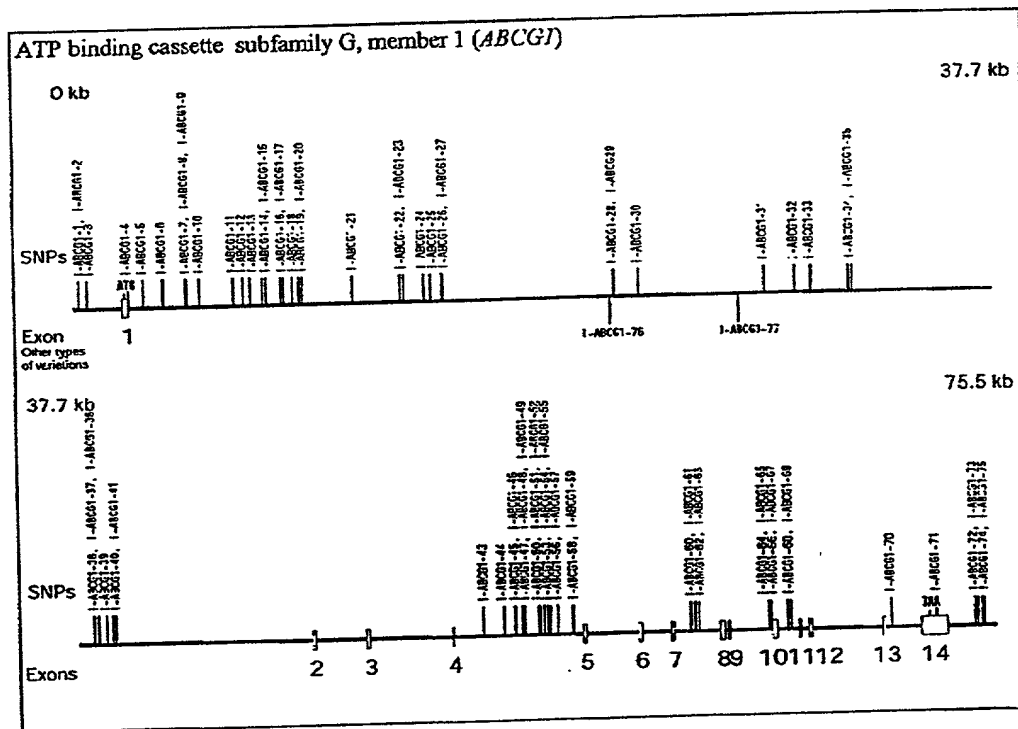


FIGURE 121

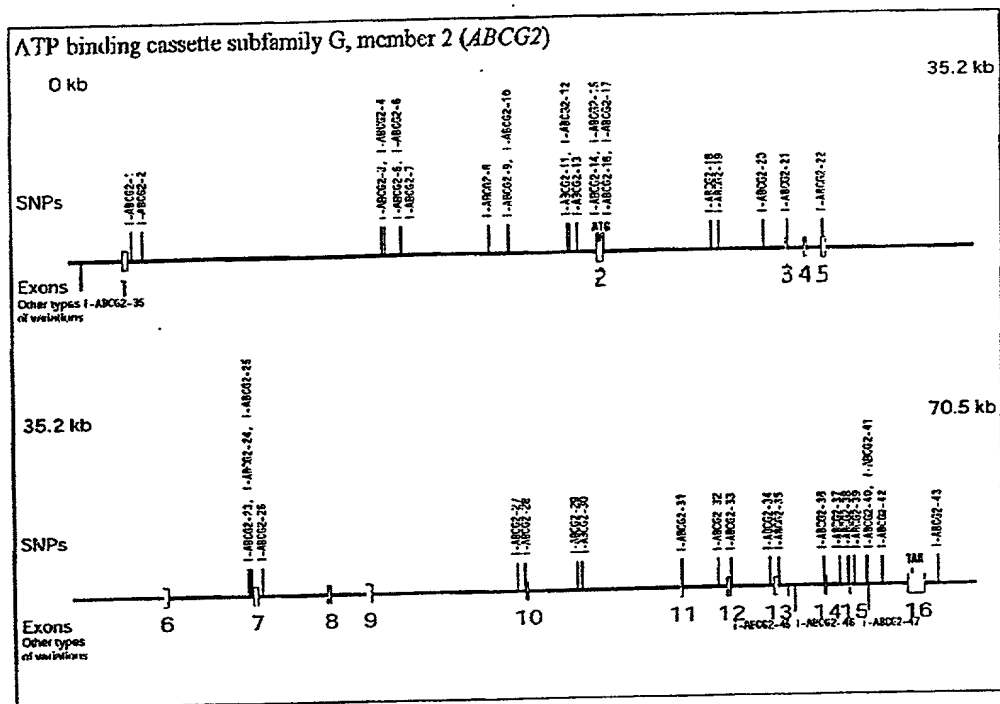


FIGURE 122

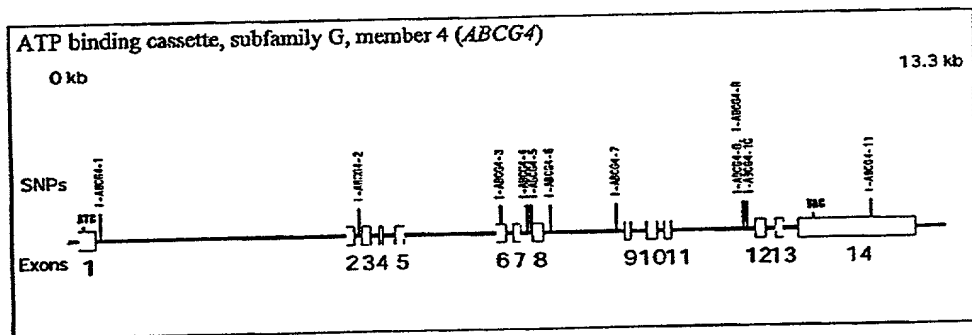


FIGURE 123

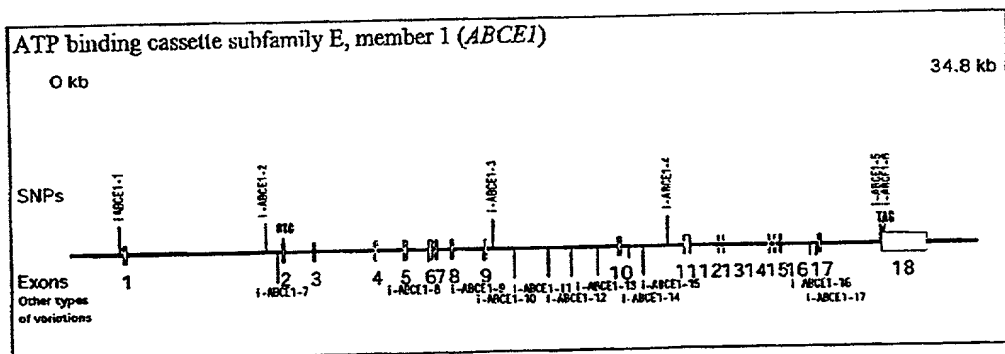


FIGURE 124

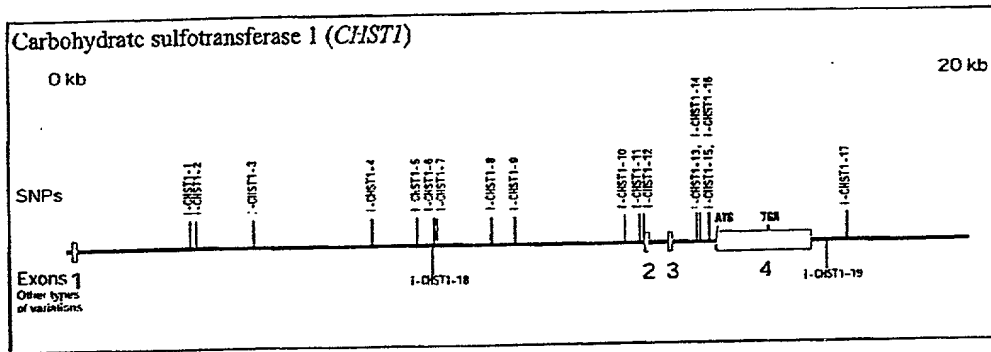


FIGURE 125

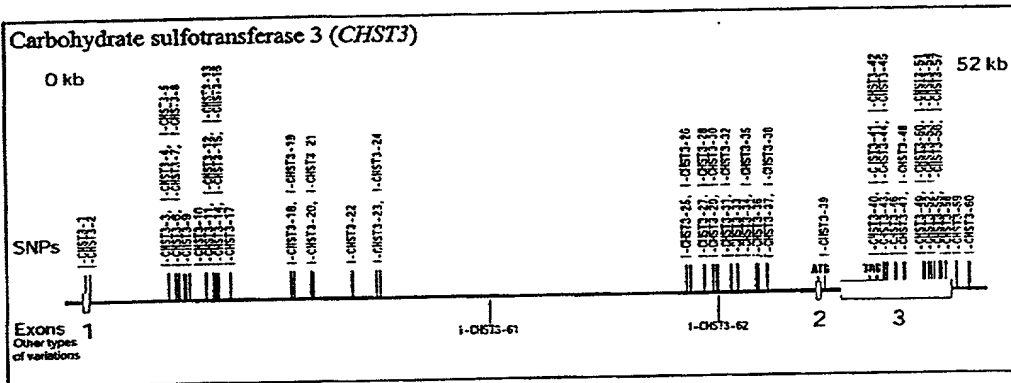


FIGURE 126

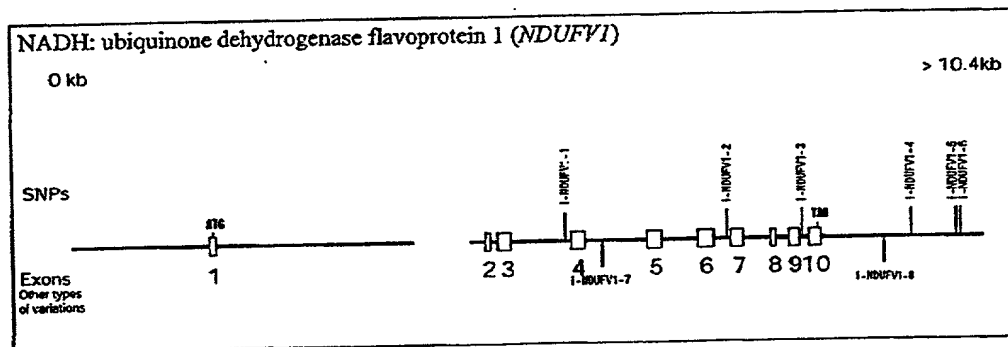




FIGURE 127

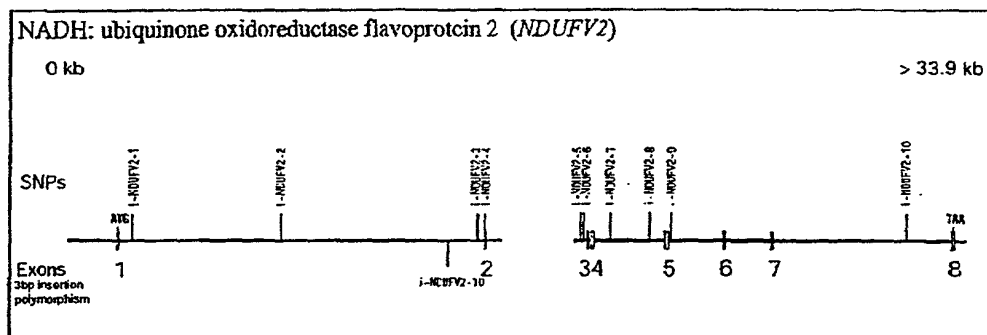


FIGURE 128

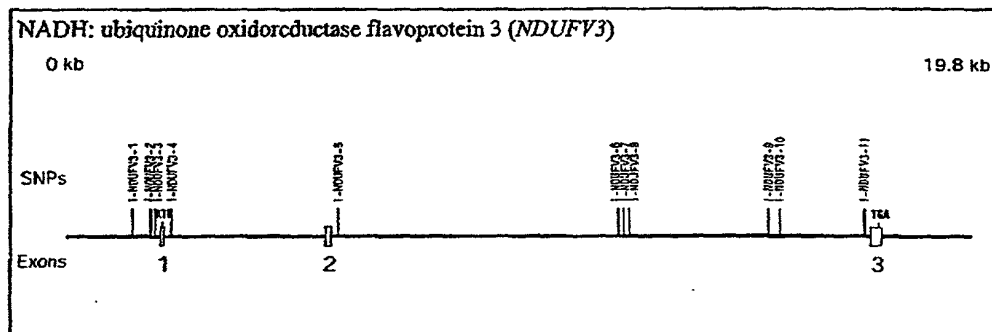


FIGURE 129

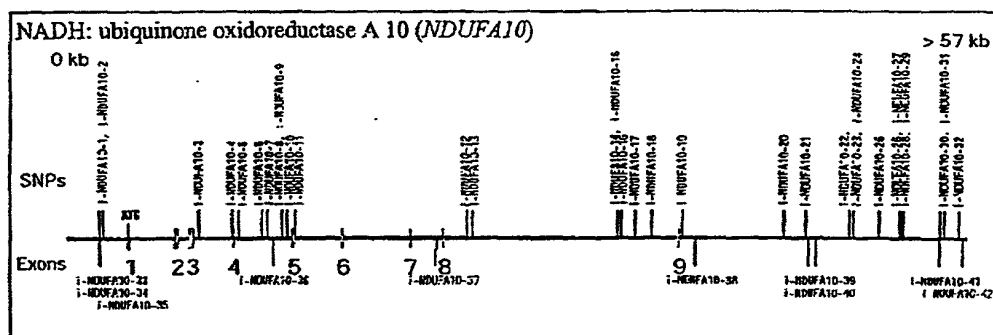


FIGURE 130

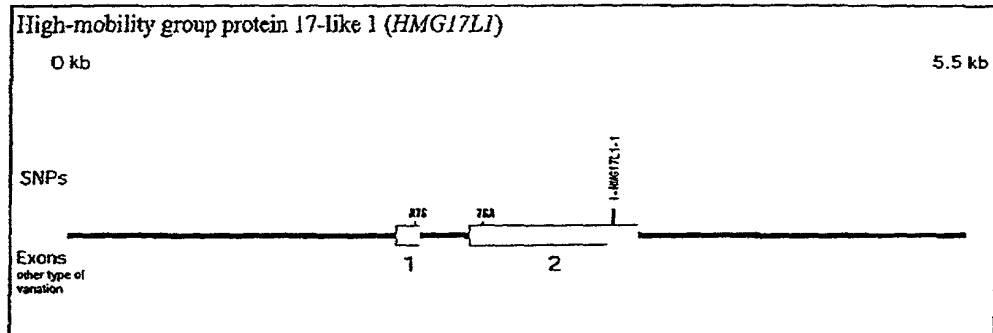


FIGURE 131

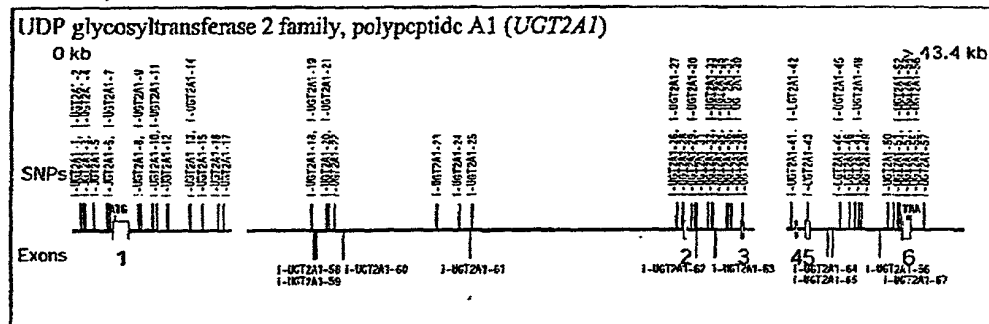


FIGURE 132

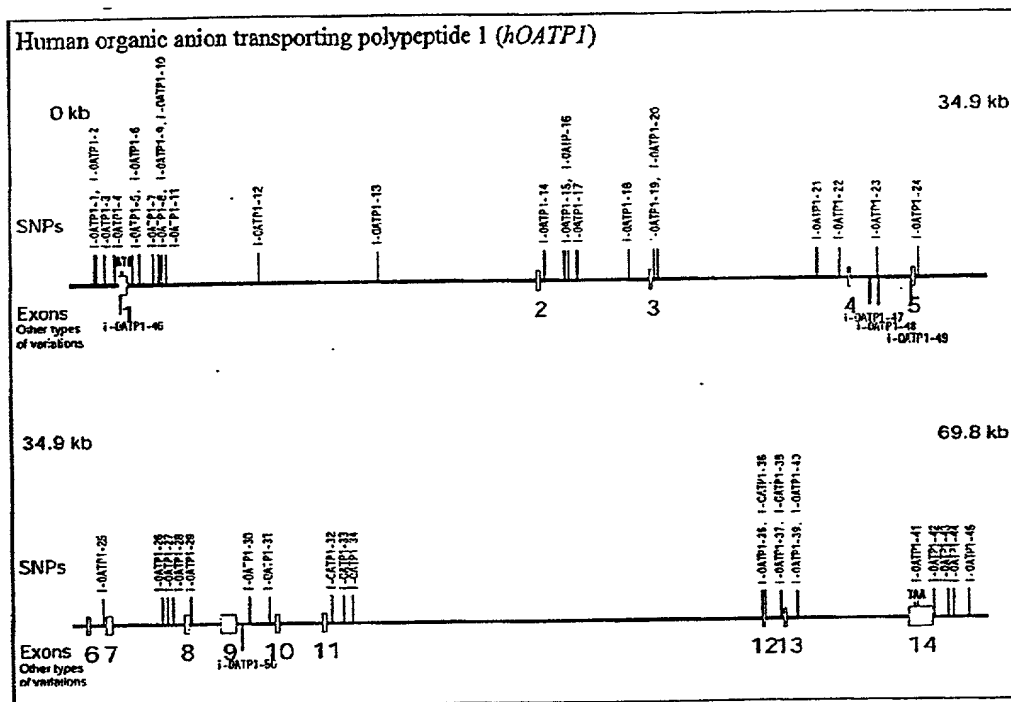




FIGURE 134

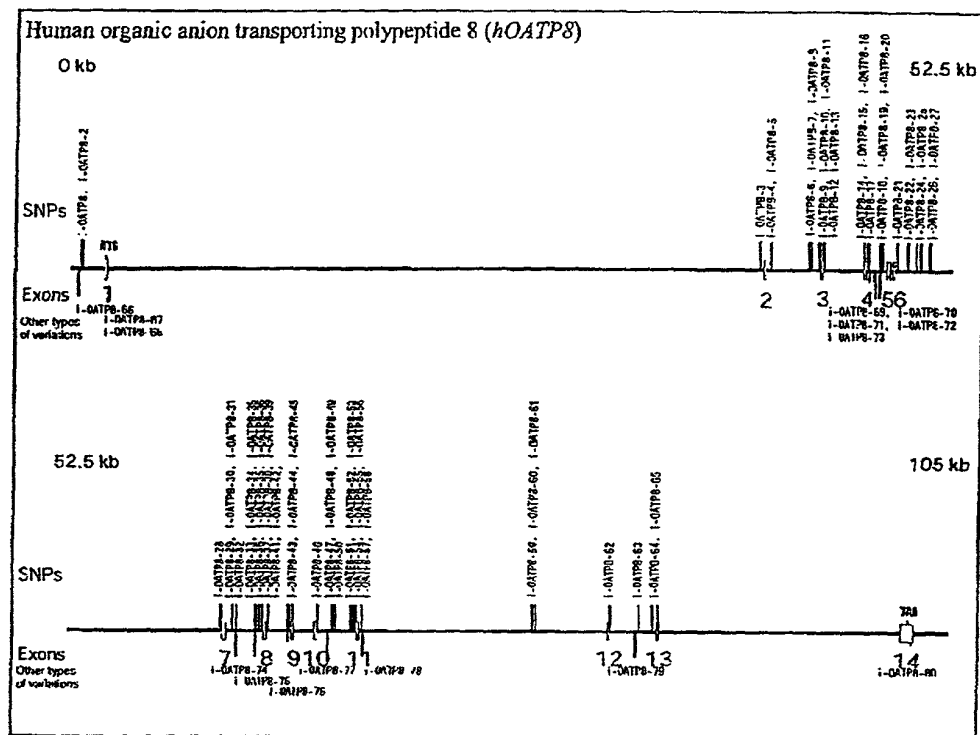


FIGURE 135

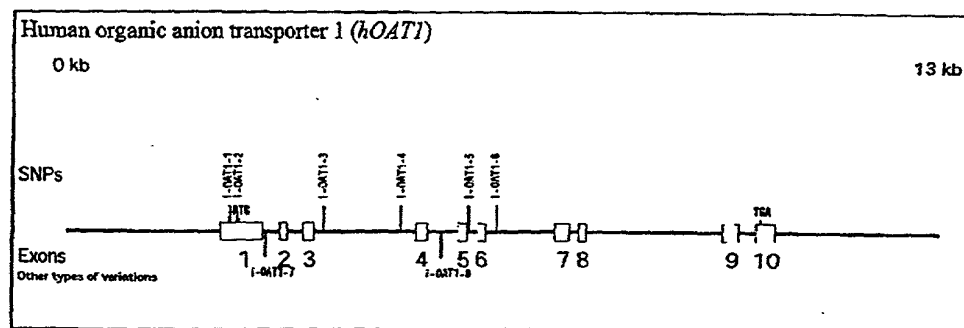


FIGURE 136

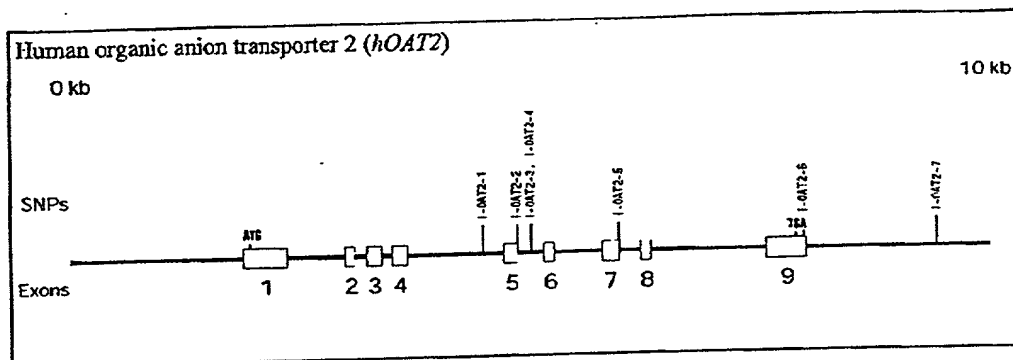
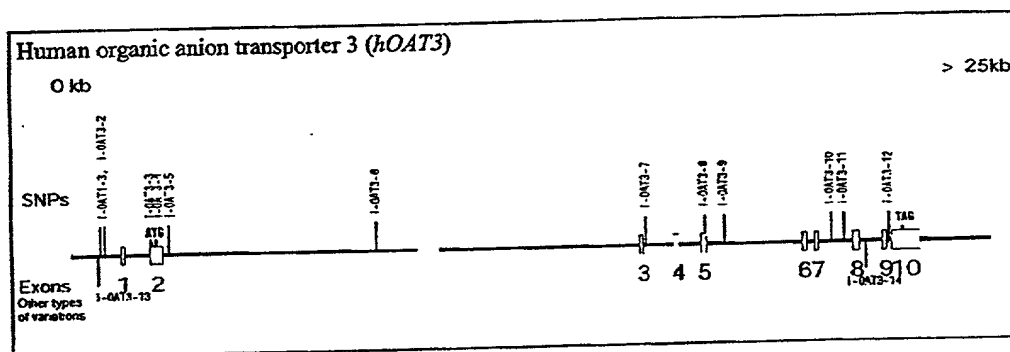
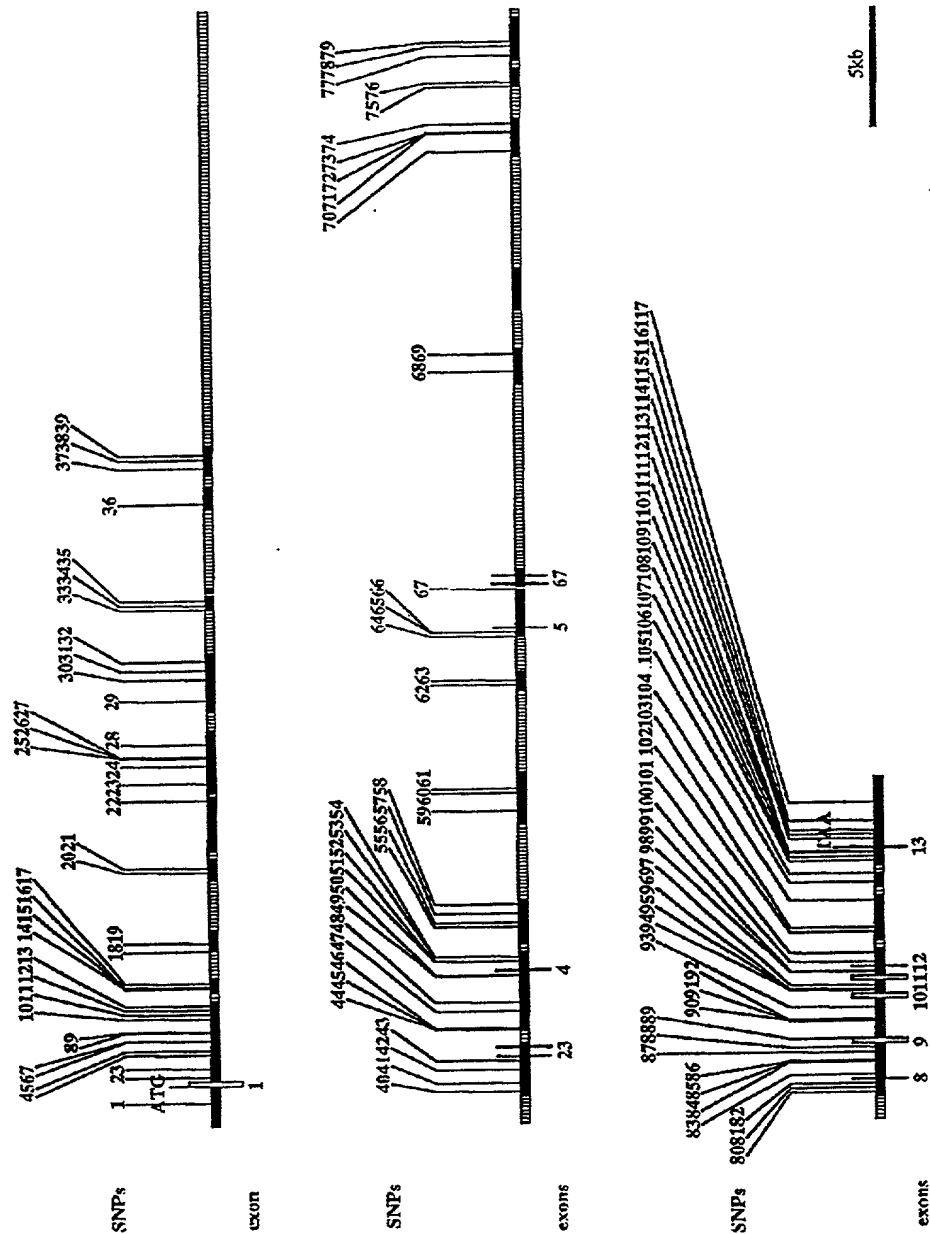


FIGURE 137



*Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2)*      ACCESSION AC025431  
AC012653



*Aldehyde dehydrogenase 1 family, member A3 (ALDH1A3)*

ACCESSION AC015712

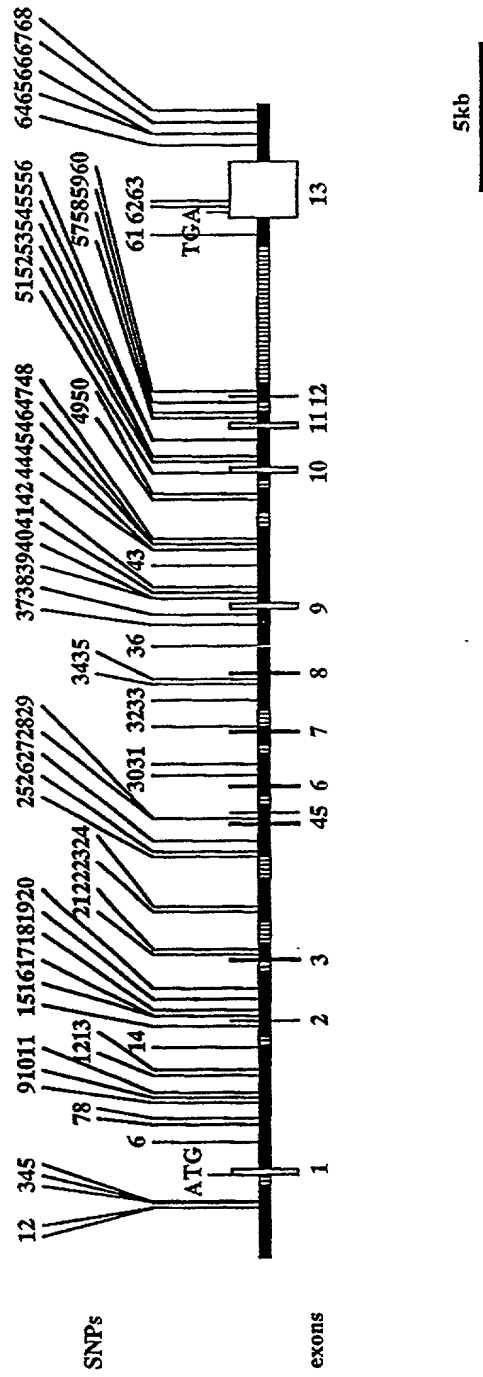


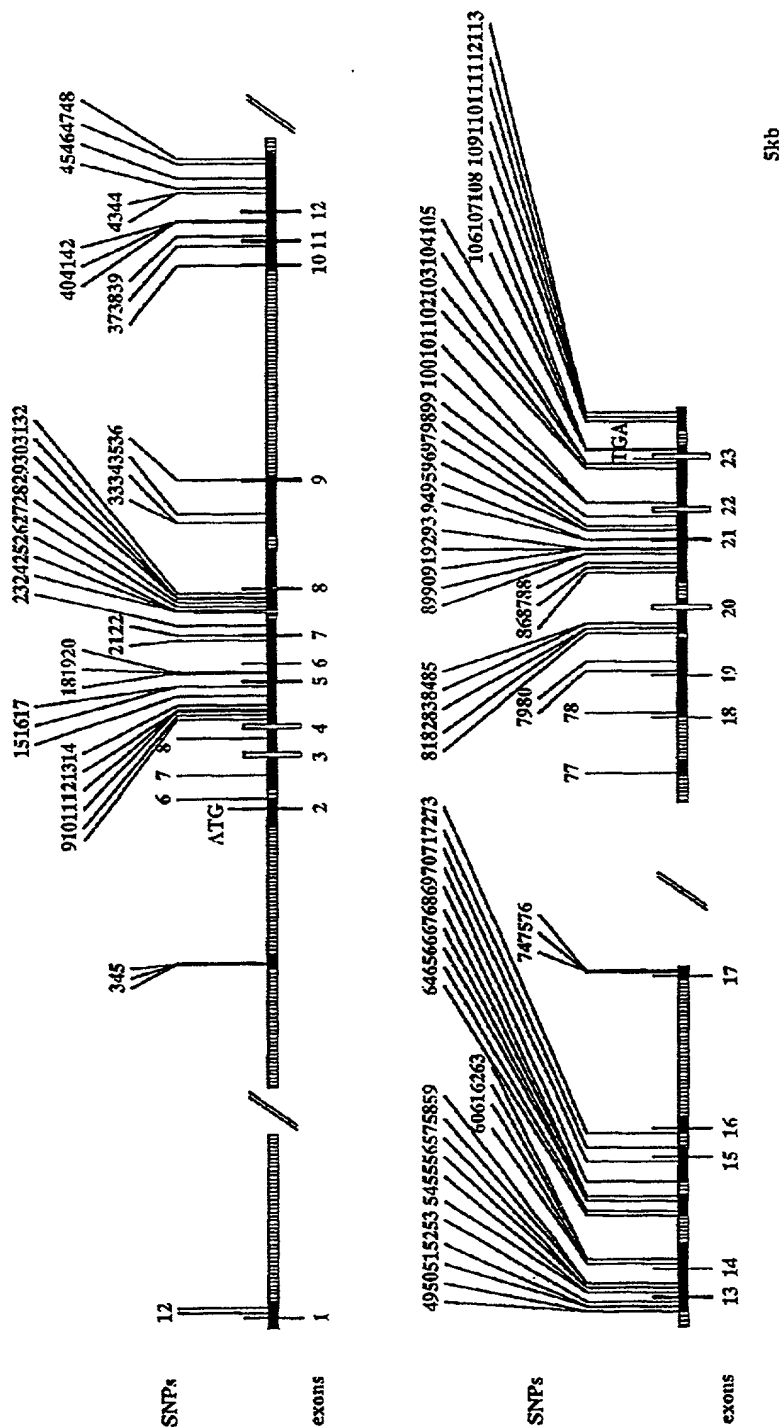
FIGURE 139



FIGURE 140

*Formyltetrahydrofolate dehydrogenase (FTHFD /ALDH1L1)*

ACCESSION AC079848



*Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)*

ACCESSION AF280107

FIGURE 141

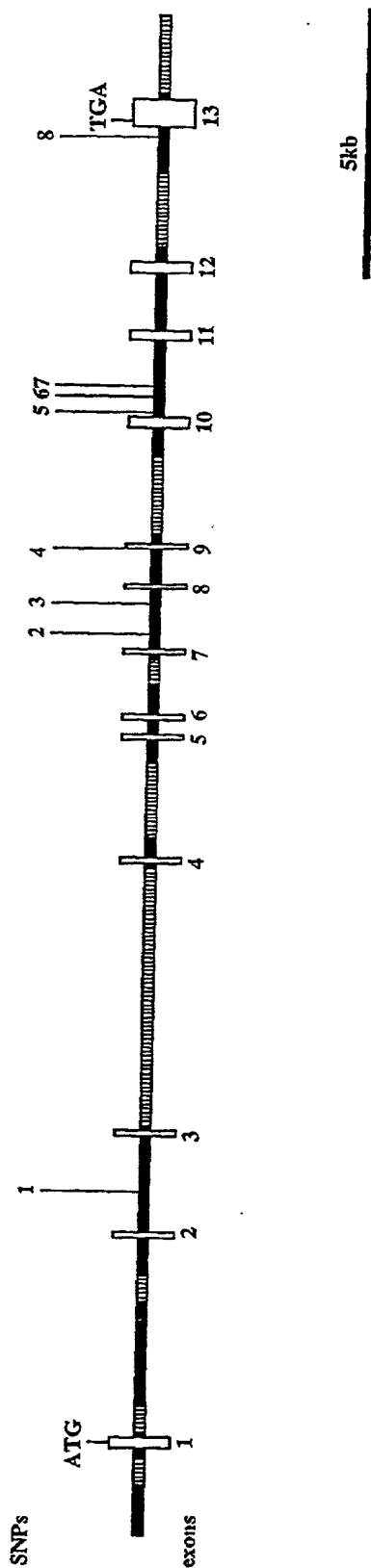
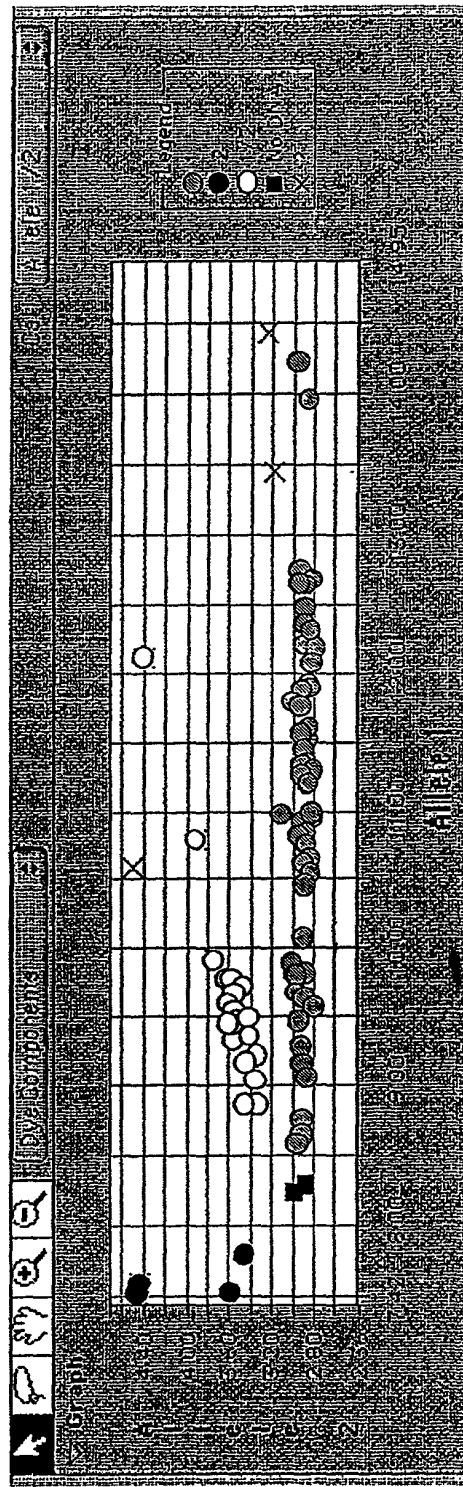
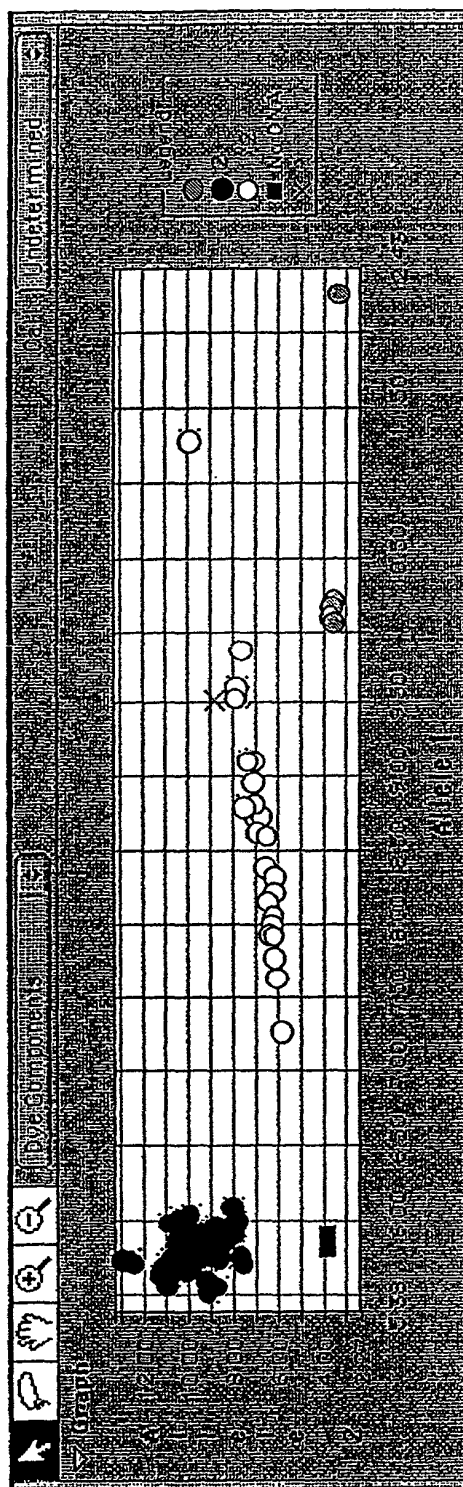


FIGURE 142



NO	GENE	LONG_GENE_NAME	CHROM.	REF. MRNA	L-LINK	OMIM_ID	EXONS	NO GENE
1	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	1
2	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	2
3	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	3
4	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	4
5	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	5
6	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	6
7	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	7
8	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	8
9	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	9
10	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	10
11	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	11
12	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	12
13	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	13
14	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	1
15	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	2
16	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	3
17	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	4
18	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	5
19	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	6
20	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	7
21	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	8
22	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	9
23	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	10
24	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	11
25	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	12
26	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	13
27	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	14
28	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	15
29	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	16
30	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	17
31	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	18
32	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	19
33	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	20
34	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	21
35	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	22
36	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	23

37	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	24
38	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	25
39	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	26
40	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	27
41	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	28
42	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	29
43	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	30
44	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	31
45	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	32
47	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	1
48	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	2
49	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	3
50	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	4
51	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	5
52	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	6
53	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	7
54	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	8
55	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	9
56	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	10
57	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	11
58	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	12
59	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	13
60	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	14
61	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	15
62	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	16
63	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	17
66	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	2
67	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	3
68	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	4
69	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	5
70	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	6
71	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	7
72	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	8
73	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	9
74	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	10
75	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	11
76	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	12

77	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	13
78	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	14
79	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	15
80	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	16
81	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	17
82	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	18
83	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	19
84	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	20
85	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	21
86	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	22
87	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	23
88	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	24
89	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	25
90	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	26
91	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	27
92	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	28
93	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	29
94	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	30
95	GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	1
96	GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	2
97	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	1
98	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	2
99	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	3
100	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	4
101	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	5
102	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	6
103	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	7
104	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	8
105	NNMT	phenylethanolamine N-methyltransferase	chr17	NM_002686	5409	171190	3	1
106	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	1
107	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	2
108	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	3
109	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	4
110	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	5
111	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	6
112	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	7
113	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	8



[illegible]



188	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	83
189	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	84
190	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	85
191	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	8
192	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	6
193	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	87
194	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	88
195	GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	1
196	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	1
197	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	2
198	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	3
199	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	4
200	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	5
201	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	6
202	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	7
203	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	8
204	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	9
205	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	10
206	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	1
218	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	13
219	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	14
221	GGT1	gamma-glutamyltransferase 1	chr22	NM_005265	2678	231950	15	
222	DIA4	NAD(P)H menadiene oxidoreductase 1,	chr16	NM_000903	1728	125860	6	1
223	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	1
224	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	2
225	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	3
226	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	1
227	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	2
228	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	3
229	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	4
230	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	5
231	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	6
232	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	7
233	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	8
234	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	9
235	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	10
236	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	11

237 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	12
238 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	13
239 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	14
240 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	15
241 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	16
242 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	17
243 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	18
244 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	19
245 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	20
246 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	21
247 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	22
248 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	23
249 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	24
250 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	25
251 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	26
252 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	27
253 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	1
254 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	2
255 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	3
256 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	4
257 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	5
258 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	6
259 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	7
260 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	8
261 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	9
262 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	10
263 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	11
264 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	12
265 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	13
266 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	14
267 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	15
268 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	16
269 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	17
270 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	18
271 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	19
272 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	20
273 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	21

274	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	22
275	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	23
276	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	24
277	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	25
278	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	1
279	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	2
280	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	3
281	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	4
282	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	5
283	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	6
284	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	7
285	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	8
286	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	9
287	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	10
288	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	11
289	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	12
290	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	13
291	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	14
292	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	15
293	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	1
294	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	2
295	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	3
296	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	4
297	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	5
298	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	6
299	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	7
300	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	8
301	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	9
302	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	10
303	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	11
304	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	12
305	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	13
306	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	14
307	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	15
308	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	16
309	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	17
310	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	18

311	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	19
312	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	20
313	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	21
314	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	22
315	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	23
316	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	24
317	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	25
318	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	26
319	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	27
320	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	28
321	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	29
322	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	30
323	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	1
324	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	2
325	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	3
326	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	4
327	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	5
328	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	6
329	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	7
330	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	8
331	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	9
332	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	10
333	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	11
334	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	12
335	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	13
336	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	14
337	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	15
338	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	16
339	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	17
340	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	18
341	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	19
342	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	1
343	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	2
344	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	3
345	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	4
346	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	5
347	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	6

348	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	7
349	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	8
350	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	9
351	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	10
352	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	11
353	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	12
354	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	13
355	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	14
356	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	15
357	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	16
358	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	17
359	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	18
360	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	19
361	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	20
362	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	21
363	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	22
364	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	23
365	SULT1A3	sulfotransferase family, cytosolic, 1A,	chr16	NM_003166	6818	600641	9	1
366	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	1
367	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	2
368	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	3
369	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	4
370	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	5
371	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	6
372	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	7
373	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	8
374	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	9
375	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	10
376	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	1
377	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	2
378	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	3
379	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	4
380	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	5
381	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	6
382	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	7
383	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	8
384	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	1

385	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	2
386	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	3
387	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	4
388	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	5
389	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	6
390	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	7
391	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	8
392	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	9
393	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	10
394	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	11
395	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	1
396	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	2
397	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	3
398	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	4
399	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	5
400	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	6
401	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	7
402	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	8
403	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	9
404	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	10
405	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	11
406	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	12
407	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	13
408	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	14
409	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	15
410	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	1
411	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	2
412	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	3
413	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	4
414	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	5
415	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	1
416	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	2
417	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	3
418	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	4
419	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	5
420	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	6
421	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	7

422	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	8
423	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	1
424	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	2
425	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	3
426	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	4
427	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	5
428	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	6
429	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	1
430	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	2
431	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	3
432	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	1
433	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	2
434	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	3
435	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	4
436	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	5
437	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	6
438	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	7
439	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	8
440	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	9
441	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	10
442	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	11
443	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	12
444	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	13
445	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	14
446	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	15
447	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	16
448	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	1
449	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	2
450	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	3
451	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	4
452	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	5
453	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	6
454	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	7
455	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	8
456	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	9
457	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	10
458	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	11

459	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	12
460	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	13
461	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	14
462	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	15
463	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	16
464	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	17
465	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	18
466	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	19
467	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	20
468	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	21
469	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	22
470	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	23
471	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	24
472	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	25
473	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	26
474	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	27
475	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	28
476	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	29
477	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	30
478	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	31
479	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	32
480	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	33
481	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	34
482	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	35
483	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	36
484	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	37
485	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	1
486	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	2
487	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	3
488	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	4
489	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	5
490	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	6
491	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	7
492	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	8
493	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	9
494	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	10
495	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	11



496 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	12
497 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	13
498 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	14
499 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	15
500 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	16
501 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	17
502 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	18
503 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	19
504 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	20
505 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	21
506 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	22
507 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	23
508 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	24
509 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	25
510 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	26
511 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	27
512 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	1
513 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	2
514 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	3
515 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	4
516 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	5
517 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	1
518 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	2
519 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	3
520 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	4
521 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	1
522 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	2
523 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	3
524 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	4
525 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	5
526 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	6
527 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	1
528 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	2
529 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	3
530 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	4
531 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	5
532 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	1

533	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	2
534	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	3
535	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	4
536	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	5
537	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	6
538	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	7
539	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	8
540	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	9
541	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	10
542	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	11
543	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	12
544	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	13
545	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	14
546	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	15
547	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	1
548	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	2
549	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	3
550	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	4
551	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	5
552	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	6
553	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	1
554	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	2
555	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	3
556	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	4
557	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	5
558	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	6
559	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	1
560	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	2
561	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	3
562	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	4
563	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	1
564	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	2
565	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	3
566	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	4
567	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	5
568	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	6
569	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	7

570	NAT1	N-acetyltransferase 1	chr8	NM_000662	9	108345	1	1
571	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	1
572	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	2
573	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	3
574	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	4
575	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	5
576	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	6
577	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	7
578	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	8
579	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	9
580	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	10
581	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	11
582	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	12
583	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	13
584	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	14
585	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	15
586	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	16
587	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	17
588	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	18
589	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	19
590	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	20
591	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	1
592	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	2
593	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	3
594	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	4
595	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	5
596	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	6
597	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	7
598	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	8
599	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	1
600	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	2
601	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	3
602	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				1
603	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				2
604	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				3
605	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				4
606	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				5

607	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	6
608	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	7
609	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	8
610	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	9
611	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	10
612	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	11
613	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	12
614	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	13
615	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	14
616	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	15
617	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	16
618	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	17
619	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	18
620	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	19
621	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	20
622	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	21
623	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	22
624	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	23
625	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	24
626	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	25
627	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158	1650	602202	11	26
628	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	4257	138330	4	1
629	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	4257	138330	4	2
630	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	4257	138330	4	3
631	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	4257	138330	4	4
632	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	4257	138330	4	5
633	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	4257	138330	4	6
634	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	4257	138330	4	7
635	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	1
636	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	2
637	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	3
638	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	4
639	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	5
640	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	6
641	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	7
642	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	8
643	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	9

Fig. 235

Sulfotransferase 1C1 (*SULT1C1*)

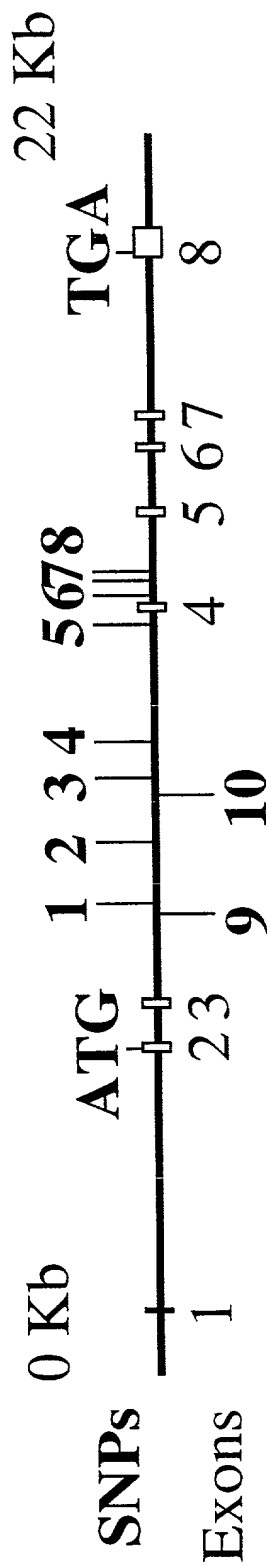
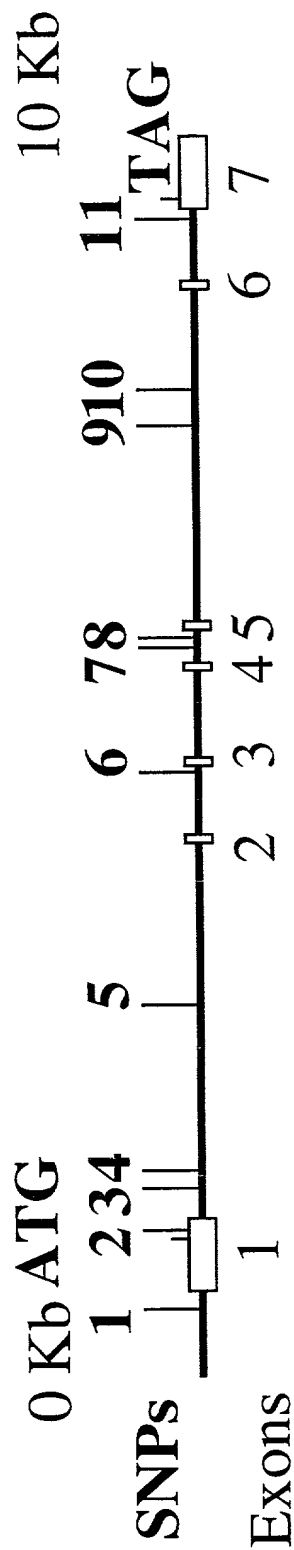


Fig. 236

Sulfotransferase 1C2 (*SULT1C2*)



680 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	16
681 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	1
682 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	2
683 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	3
684 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	4
685 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	5
686 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	6
687 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	7
688 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	8
689 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	9
690 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	10
691 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	11
692 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	12
693 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	13
694 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	14
695 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	15
696 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	16
697 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	17
698 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	18
699 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	19
700 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	20
701 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	21
702 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	1
703 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	2
704 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	3
705 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	4
706 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	5
707 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	6
708 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	7
709 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	8
710 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	9
711 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	10
712 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	2
713 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	3
714 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	4
715 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	5
716 GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	1

717 GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	2
718 GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	3
719 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	1
720 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	2
721 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	3
722 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	4
723 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	5
724 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	6
725 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	7
726 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	8
727 GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	9
728 GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	1
729 GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	2
730 GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	3
731 GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	4
732 GSTT1	glutathione S-transferase theta 1	chr22	NM_000853	2952	600436	5	1
733 PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	1
734 PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	2
735 PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	3
736 PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	4
737 PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	5
738 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	1
739 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	2
740 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	3
741 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	4
742 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	5
743 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	6
744 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	7
745 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	8
746 MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	9
747 MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	1
748 MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	2
749 MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	3
750 MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	4
751 MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	5
752 MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	6
753 MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	7

Observed	:	T/C
3' Assay	:	ACAAGCCATT GCGCTAGAGA GAGCCATCTG CAGTTTCTCC TTAGACAGAT GTTCAGATGG
Comment	:	
Sample size	:	96

## Screened Sequence

Accession No.	:	NT_024413.3 (Graphical View of this Entry)
Chromosome	:	12
map	:	
Definition of the record	:	Homo sapiens chromosome 12 working draft sequence segment.
Position in sequence	:	536287 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID	:	NT_024413.3_20010417_1	
Amplified region	:	536137..536950 in NT_024413	
size	:	814	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTGAGAACAT GAGGCAGTGT	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104892](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892)

12/17/2001



791	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha	chrX	NM_004541	4694	300078	3	5
792	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	1
793	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	2
794	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	3
795	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	4
796	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	5
797	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	6
798	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	6
799	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_004542	4696	603832	4	1
800	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_004542	4696	603832	4	2
801	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_004542	4696	603832	4	3
802	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	1
803	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	2
804	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	3
805	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	4
806	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	5
807	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	5
808	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	6
809	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	7
810	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	1
811	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	2
812	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	3
813	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	4
814	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	5
815	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	6
816	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	6
817	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	1
818	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	2
819	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	3
820	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	4
821	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	5
822	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	6
823	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	7
824	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	8
825	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	9
826	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	10
827	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	11

828	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	12
829	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	12
830	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	13
831	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	14
832	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	1
833	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	2
834	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	3
835	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	4
836	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	5
837	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	6
838	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	7
839	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	8
840	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	9
841	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	10
842	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	11
843	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	12
844	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	12
845	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	13
846	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	13
847	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta	chr16	NM_005003	4706	603836	5	1
848	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta	chr16	NM_005003	4706	603836	5	2
849	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	1
850	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	2
851	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	3
852	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	4
853	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	5
854	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	6
855	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	7
856	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	8
857	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	9
858	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	10
859	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	11
860	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	12
861	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	13
862	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	14
863	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	15
864	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	16

865	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	17
866	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	18
867	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	19
868	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	20
869	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	21
870	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	22
871	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	23
872	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	24
873	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	25
874	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	26
875	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	27
876	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	28
877	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	29
878	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	30
879	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	31
880	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	32
881	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	33
882	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	34
883	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	35
884	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	36
885	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	37
886	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	38
887	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	39
888	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	40
889	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	40
890	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	41
891	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	1
892	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	2
893	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	3
894	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	4
895	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	5
896	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	6
897	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	7
898	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	8
899	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	9
900	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	10
901	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	11

# SNP Information for IMS-JST104848

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST104848  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_028388.2	301178	19	71733798

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011148.3	genomic	NDUFA3	CDS*1	Annotated	

939	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	6
940	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	7
941	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	8
942	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	9
943	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	10
944	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	11
945	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	12
946	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	13
947	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	14
948	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	15
949	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	16
950	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	17
951	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	18
952	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	19
953	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	20
954	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	21
956	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	22
957	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	24
958	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	1
959	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	2
960	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	3
961	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	4
962	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	5
963	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	6
964	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	7
965	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	8
966	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	9
967	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	10
968	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	11
969	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	12
970	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	13
971	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	14
972	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	15
973	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	16
974	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	17
975	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	18
976	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	19

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : GTAGATGGAA GATAGTAGGC A  
BackwardPrimer : AGGATCAGTT CCATTCTGC AC



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104949](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104949)

12/17/2001

[illegible]

[illegible]





[illegible]

1162	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	161
1163	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	162
1164	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	163
1165	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	163
1166	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	164
1167	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	165
1168	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	166
1169	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	167
1170	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	167
1171	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	168
1172	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	168
1173	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	169
1174	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	169
1175	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	170
1176	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	1
1177	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	2
1178	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	3
1179	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	4
1180	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	5
1181	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	6
1182	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	7
1183	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	8
1184	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	9
1185	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	10
1186	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	11
1187	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	12
1188	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	13
1189	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	14
1190	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	15
1191	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	16
1192	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	17
1193	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	1
1194	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	2
1195	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	3
1196	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	4
1197	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	5
1198	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	6

1199	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	7
1200	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	8
1201	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	9
1202	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	10
1203	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	11
1204	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	12
1205	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	12
1206	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	13
1207	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	14
1207	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	14
1209	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	15
1210	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	16
1211	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	16
1212	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	17
1213	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	18
1214	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	19
1215	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	20
1216	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	21
1217	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	22
1218	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	23
1219	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	24
1220	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	25
1221	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	26
1222	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	27
1223	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	28
1224	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	29
1225	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	30
1226	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	31
1227	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	32
1228	GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	3
1229	PNMT	phenylethanolamine N-methyltransferase	chr17	NM_002686	5409	171190	3	2
1230	CYP1A1	cytochrome P450, subfamily I (aromatic	chr15	NM_000499	1543	108330	7	1
1231	CYP1A1	cytochrome P450, subfamily I (aromatic	chr15	NM_000499	1543	108330	7	2
1232	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	1
1233	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	2
1234	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	3
1235	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	4

1236 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	5
1237 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	6
1238 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	1
1239 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	2
1240 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	3
1241 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	4
1242 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	5
1243 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	6
1244 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	7
1245 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	8
1246 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	8
1247 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	9
1248 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	10
1249 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	11
1250 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	11
1251 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	12
1252 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	90
1253 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	91
1254 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	92
1255 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	93
1256 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	94
1257 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	95
1258 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	96
1259 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	97
1260 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	98
1261 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	21
1262 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	22
1263 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	23
1264 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	24
1265 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	25
1266 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	26
1267 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	27
1268 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	1
1269 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	2
1270 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	3
1271 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	4
1272 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	5

1273 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	6
1274 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	7
1275 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	8
1276 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	9
1277 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	10
1278 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	11
1279 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	12
1280 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	13
1281 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	14
1282 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	15
1283 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	16
1284 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	17
1285 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	18
1286 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	19
1287 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	20
1288 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	21
1289 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	22
1290 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	1
1291 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	2
1292 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	3
1293 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	4
1294 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	5
1295 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	6
1296 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	7
1297 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	8
1298 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	9
1299 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	10
1300 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	11
1301 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	12
1302 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	13
1303 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	14
1304 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	15
1305 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	16
1306 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	17
1307 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	18
1308 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	19
1309 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	20

1310 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	21
1311 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	22
1312 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	23
1313 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	24
1314 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	25
1315 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	26
1316 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	27
1317 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	28
1318 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	29
1319 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	30
1320 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	31
1321 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	32
1322 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	33
1323 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	34
1324 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	35
1325 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	36
1326 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	37
1327 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	38
1328 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	39
1329 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	40
1330 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	41
1331 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	8
1332 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	9
1333 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	10
1334 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	11
1335 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	12
1336 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	13
1337 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	14
1338 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	15
1339 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	1
1340 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	2
1341 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	3
1342 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	4
1343 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	5
1344 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	6
1345 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	7
1346 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	8

[illegible]



1384 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	4
1385 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	5
1386 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	6
1387 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	7
1388 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	8
1389 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	9
1390 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	10
1391 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	11
1392 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	12
1393 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	13
1394 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	14
1395 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	15
1396 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	16
1397 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	17
1398 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	18
1399 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	19
1400 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	20
1401 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	21
1402 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	22
1403 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	23
1404 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	24
1405 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	25
1406 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	26
1407 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	27
1408 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	28
1409 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	29
1410 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	30
1411 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	31
1412 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	32
1413 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	33
1414 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	34
1415 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	35
1416 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	36
1417 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	37
1418 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	37
1419 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	38
1421 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	1

1422 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	2
1423 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	3
1424 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	4
1425 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	5
1426 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	6
1427 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	1
1428 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	2
1429 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	3
1430 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	4
1431 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	5
1432 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	6
1433 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	7
1434 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	8
1435 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	9
1436 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	10
1437 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	10
1438 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	11
1439 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	12
1440 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	13
1441 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	14
1442 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	15
1443 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	1
1444 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	2
1445 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	3
1446 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	4
1447 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	5
1448 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	6
1449 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	7
1450 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	8
1451 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	9
1452 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	10
1453 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	11
1454 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	12
1455 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	13
1456 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	14
1457 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	14
1458 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	15

1459 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	16
1460 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	17
1461 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	18
1462 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	19
1463 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	20
1464 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	21
1465 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	22
1466 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	1
1467 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	2
1468 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	3
1469 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	4
1470 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	5
1471 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	6
1472 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	7
1473 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	8
1474 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	9
1475 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	10
1476 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	11
1477 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	12
1478 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	13
1479 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	14
1480 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	15
1481 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	16
1482 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	17
1483 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	1
1484 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	2
1485 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	3
1486 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	4
1487 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	5
1488 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	6
1489 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	7
1490 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	8
1491 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	9
1492 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	10
1493 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	11
1494 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	1
1495 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	1

[illegible]





1609 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	29
1610 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	30
1611 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	31
1612 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	32
1613 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	33
1614 CYP27A1	cytochrome P450, subfamily XXVIIA, polypeptide 1	chr2	NM_000784	1593	213700	9	1
1615 CYP27A1	cytochrome P450, subfamily XXVIIA, polypeptide 1	chr2	NM_000784	1593	213700	9	2
1616 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	1
1617 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	2
1618 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	3
1619 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	4
1620 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	5
1621 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	6
1622 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	7
1623 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	8
1624 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	9
1625 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	10
1626 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	11
1627 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	12
1628 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	13
1629 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	14
1630 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	15
1631 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	16
1632 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	17
1633 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	18
1634 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	19
1635 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	20
1636 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	21
1637 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	22
1638 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	23
1639 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	23
1640 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	24
1641 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	25
1642 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	26
1643 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	27
1644 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	28
1645 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	29





1683 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	4
1684 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	5
1685 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	6
1686 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	7
1687 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	8
1688 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	9
1689 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	10
1690 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	11
1691 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	11
1692 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	12
1693 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	13
1694 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	14
1695 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	15
1696 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	16
1697 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	17
1698 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	18
1699 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	19
1700 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	20
1701 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	21
1702 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	1
1703 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	2
1704 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	3
1705 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	4
1706 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	5
1707 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	6
1708 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	7
1709 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	8
1710 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	9
1711 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	10
1712 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	11
1713 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	12
1714 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	13
1715 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	14
1716 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	15
1717 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	16
1718 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	17
1719 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	17

1720	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	18
1721	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	19
1722	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	20
1723	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	1
1724	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	2
1725	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	3
1726	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	4
1727	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	5
1728	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	6
1729	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	7
1730	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	8
1731	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	1
1732	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	2
1733	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	3
1734	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	4
1735	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	5
1736	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	6
1737	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	7
1738	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	8
1739	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	9
1740	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	10
1741	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	11
1742	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	12
1743	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	13
1744	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	14
1745	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	15
1746	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	16
1747	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	17
1748	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	18
1749	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	19
1750	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	20
1751	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	21
1752	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	22
1753	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	23
1754	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	24
1755	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	25
1756	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	26

1757	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	27
1758	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	28
1759	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	29
1760	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	30
1761	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	31
1762	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	1
1763	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	2
1764	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	3
1765	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	4
1766	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	5
1767	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	6
1768	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	7
1769	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	8
1770	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	9
1771	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	10
1772	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	10
1773	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	11
1774	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	12
1775	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	13
1776	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	14
1777	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	15
1778	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	1
1779	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	2
1780	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	3
1781	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	4
1782	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	5
1783	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	6
1784	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	7
1785	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	8
1786	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	9
1787	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	10
1788	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	11
1789	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	12
1790	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	13
1791	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	14
1792	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	15
1793	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	16

Fig. 209 Alcohol dehydrogenase 1 (*ADH1*)

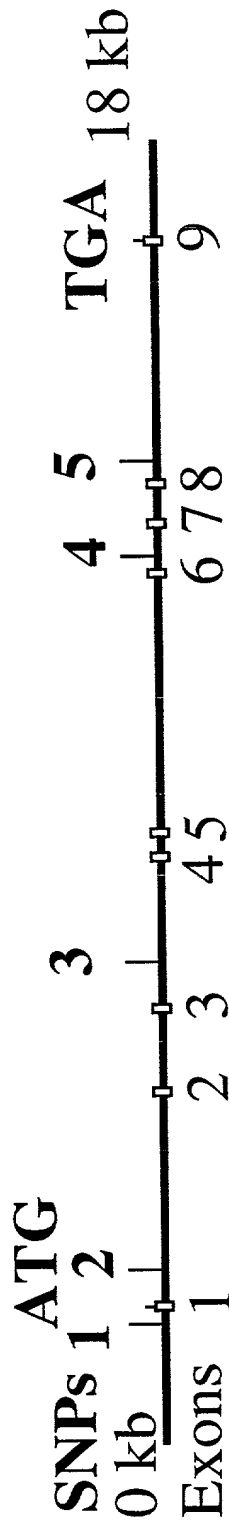


Fig. 210 Alcohol dehydrogenase 2 (*ADH2*)

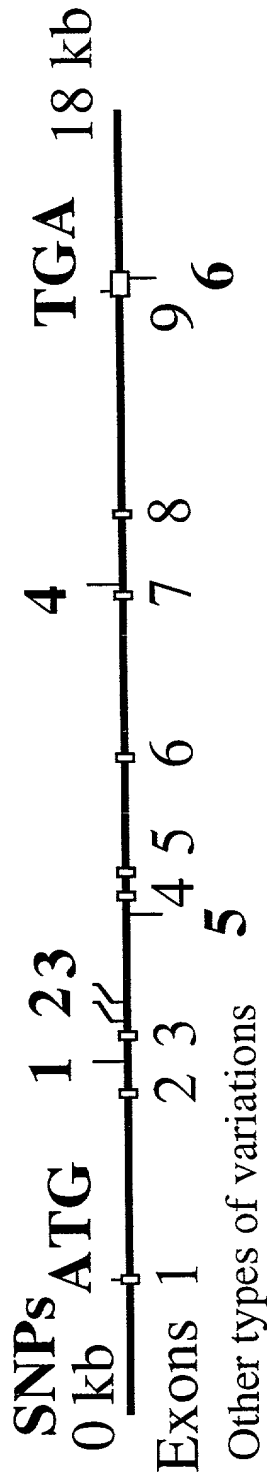
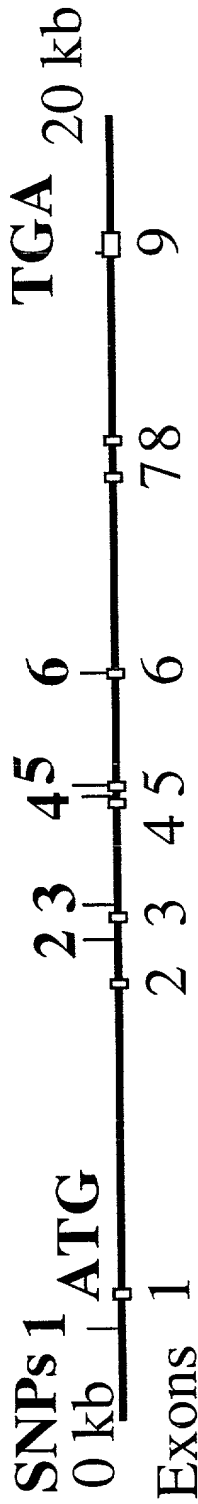


Fig. 211 Alcohol dehydrogenase 3 (*ADH3*)





1869 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	45
1870 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	46
1871 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	47
1872 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	48
1873 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	49
1874 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	50
1875 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	51
1876 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	52
1877 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	53
1878 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	54
1879 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	55
1880 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	56
1881 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	57
1882 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	58
1883 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	1
1884 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	2
1885 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	3
1886 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	4
1887 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	5
1888 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	6
1889 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	7
1890 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	8
1891 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	9
1892 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	10
1893 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	11
1894 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	12
1895 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	13
1896 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	14
1897 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	15
1898 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	16
1899 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	17
1900 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	18
1901 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	19
1902 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	20
1903 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	21
1904 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	22
1905 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	



[illegible]





# TABLE "EESOOT"

2017	ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	44
2018	ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	45
2019	ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	46
2020	ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	47
2021	ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	48
2022	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	1
2023	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	2
2024	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	3
2025	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	4
2026	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	5
2027	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	6
2028	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	7
2029	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	8
2030	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	9
2031	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	10
2032	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	11
2033	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	12
2034	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	13
2035	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	14
2036	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	15
2037	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	16
2038	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	17
2039	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	18
2040	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	19
2041	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	20
2042	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	21
2043	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	21
2044	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	22
2045	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	23
2046	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	24
2047	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	25
2048	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	26
2049	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	27
2050	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	28
2051	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	29
2052	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	30
2053	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	31

2054	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	32
2055	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	33
2056	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	34
2057	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	35
2058	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	36
2059	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	37
2060	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	38
2061	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	39
2062	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	40
2063	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	41
2064	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	42
2065	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	43
2066	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	44
2067	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	45
2068	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	46
2069	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	47
2070	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	48
2071	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	49
2072	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	33
2073	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	23
2074	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	24
2075	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	1
2076	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	2
2077	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	3
2078	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	4
2079	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	5
2080	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	6
2081	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	7
2082	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	8
2083	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	9
2084	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	10
2085	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	11
2086	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	12
2087	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	13
2088	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	14
2089	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	15
2090	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	16

[illegible]



[illegible][illegible]







2277 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	199
2278 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	200
2279 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	201
2280 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	202
2281 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	1
2282 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	2
2283 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	3
2284 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	4
2285 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	5
2286 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	6
2287 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	7
2288 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	8
2289 BCCA7							9
2290 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	10
2291 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	11
2292 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	12
2293 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	13
2294 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	14
2295 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	15
2296 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	16
2297 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	17
2298 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	18
2299 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	19
2300 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	20
2301 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	21
2302 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	22
2303 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	23
2304 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	24
2305 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	25
2306 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	26
2307 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	27
2308 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	28
2309 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	29
2310 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	30
2311 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	31
2312 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	32
2313 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	33



2351 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	71
2352 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	1
2353 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	2
2354 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	3
2355 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	4
2356 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	5
2357 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	6
2358 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	7
2359 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	8
2360 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	9
2361 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	10
2362 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	11
2363 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	12
2364 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	13
2365 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	14
2366 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	15
2367 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	16
2368 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	17
2369 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	18
2370 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	19
2371 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	20
2372 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	21
2373 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	22
2374 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	23
2375 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	24
2376 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	25
2377 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	26
2378 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	27
2379 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	28
2380 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	29
2381 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	30
2382 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	31
2383 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	32
2384 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	33
2385 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	34
2386 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	35
2387 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	36



2425 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	74
2426 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	75
2427 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	76
2428 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	77
2429 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	78
2430 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	79
2431 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	1
2432 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	2
2433 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	3
2434 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	4
2435 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	5
2436 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	6
2437 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	7
2438 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	8
2439 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	9
2440 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	10
2441 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	11
2442 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	12
2443 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	13
2444 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	14
2445 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	15
2446 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	16
2447 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	17
2448 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	18
2449 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	19
2450 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	20
2451 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	21
2452 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	22
2453 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	23
2454 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	24
2455 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	25
2456 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	26
2457 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	27
2458 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	28
2459 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	29
2460 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	30
2461 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	31

2462 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	32
2463 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	33
2464 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	34
2465 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	35
2466 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	36
2467 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	37
2468 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	38
2469 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	39
2470 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	40
2471 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	41
2472 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	42
2473 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	43
2474 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	44
2475 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	45
2476 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	46
2477 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	47
2478 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	1
2479 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	2
2480 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	3
2481 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	4
2482 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	5
2483 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	6
2484 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	7
2485 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	8
2486 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	9
2487 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	10
2488 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	11
2489 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	1
2490 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	2
2491 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	3
2492 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	4
2493 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	5
2494 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	6
2495 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	7
2496 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	8
2497 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	9
2498 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	10

2499 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	11
2500 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	11
2501 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	12
2502 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	13
2503 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	14
2504 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	15
2505 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	16
2506 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	17
2507 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	1
2508 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	2
2509 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	3
2510 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	4
2511 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	5
2512 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	6
2513 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	7
2514 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	8
2515 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	9
2516 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	10
2517 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	11
2518 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	12
2519 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	13
2520 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	14
2521 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	15
2522 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	16
2523 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	17
2524 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	18
2525 CHST1	carbohydate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	19
2526 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	1
2527 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	2
2528 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	3
2529 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	4
2530 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	5
2531 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	6
2532 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	7
2533 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	8
2534 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	9
2535 CHST3	carbohydate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	10





# Footnote

Observed : A/G  
 3' Assay : CCGTGGTTCA TGCCTGTAAT CCGAGCACTA TGGGAGGCGG AGACGGGCGG ATCACCAGGT  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011190.3 (Graphical View of this Entry)  
 Chromosome : 19  
 map  
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
 Position in Sequence : 1120657 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_011190.3.20010417\_4  
 Amplified region : 1120220..1121152 in NT\_011190  
 size : 933

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGTGAATAAC TATGTACCA	G

2610	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	3
2611	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	4
2612	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	5
2613	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	6
2614	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	7
2615	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	8
2616	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	9
2617	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	10
2618	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	11
2619	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	1
2620	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	2
2621	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	3
2622	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	4
2623	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	5
2624	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	6
2625	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	7
2626	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	8
2627	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	9
2628	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	10
2629	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	11
2630	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	12
2631	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	13
2632	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	14
2633	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	15
2634	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	16
2635	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	17
2636	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	18
2637	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	19
2638	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	20
2639	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	21
2640	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	22
2641	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	23
2642	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	24
2643	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	25
2644	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	26
2645	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	27
2646	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	28

2647	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	29
2648	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	30
2649	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	31
2650	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	32
2651	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	33
2652	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	34
2653	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	35
2654	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	36
2655	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	37
2656	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	37
2657	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	38
2658	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	39
2659	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	40
2660	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	40
2661	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	41
2662	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	42
2663	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	37
2664	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	38
2665	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	39
2666	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	40
2667	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	41
2668	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	42
2669	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	43
2670	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	44
2671	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	45
2672	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	46
2673	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	47
2674	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	48
2675	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	49
2676	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	50
2677	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	51
2678	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	52
2680	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	54
2681	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	55
2682	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	56
2683	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	57
2684	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	58

2685	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	59
2686	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	60
2687	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	61
2688	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	62
2689	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	63
2690	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	64
2691	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	65
2692	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	66
2693	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	67
2694	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	68
2695	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	69
2696	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	70
2697	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	71
2698	HMG17L1	high-mobility group (nonhistone chromosomal)	chr22	NM_021024	23605	0	2	1
2699	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	1
2700	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	2
2701	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	3
2702	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	4
2703	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	5
2704	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	6
2705	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	7
2706	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	8
2707	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	9
2708	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	10
2709	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	11
2710	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	12
2711	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	13
2712	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	14
2713	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	15
2714	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	16
2715	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	17
2716	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	18
2717	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	19
2718	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	20
2719	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	21
2720	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	22
2721	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	23



2759	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	61
2760	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	62
2761	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	63
2762	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	64
2763	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	65
2764	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	66
2765	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	1
2766	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	2
2767	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	3
2768	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	4
2769	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	5
2770	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	6
2771	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	7
2772	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	8
2773	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	9
2774	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	10
2775	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	11
2776	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	12
2777	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	13
2778	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	14
2779	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	15
2780	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	16
2781	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	17
2782	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	18
2783	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	19
2784	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	20
2785	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	21
2786	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	22
2787	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	23
2788	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	24
2789	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	25
2790	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	26
2791	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	27
2792	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	28
2793	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	29
2794	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	30
2795	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	31

2796	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	32
2797	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	33
2798	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	34
2799	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	35
2800	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	36
2801	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	37
2802	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	38
2803	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	39
2804	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	40
2805	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	41
2806	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	42
2807	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	43
2808	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	44
2809	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	45
2810	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	46
2811	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	47
2812	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	48
2813	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	49
2814	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	50
2815	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	51
2816	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	1
2817	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	2
2818	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	3
2819	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	4
2820	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	5
2821	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	6
2822	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	7
2823	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	8
2824	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	9
2825	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	10
2826	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	11
2828	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	12
2829	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	14
2830	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	15
2831	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	16
2832	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	17
2833	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	18





PCR "SEQUENCE"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TCTTCAGGTA CTCTTACCTA G  
BackwardPrimer : CGTGCCTTCTA CCTTCTATTA C



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104980](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104980)

2908 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	93
2909 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	94
2910 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	95
2911 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	96
2912 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	97
2913 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	98
2914 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	99
2915 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	100
2916 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	101
2917 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	102
2918 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	103
2919 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	104
2920 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	105
2921 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	106
2922 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	107
2923 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	108
2924 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	109
2925 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	110
2926 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	111
2927 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	112
2928 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	113
2929 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	114
2930 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	115
2931 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	116
2932 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	117
2933 SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	118
2934 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	1
2935 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	2
2936 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	3
2937 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	4
2938 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	5
2939 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	6
2940 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	7
2941 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	8
2942 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	9
2943 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	10
2944 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	11

[illegible]

[illegible]

3020	SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	6
3021	NAT1	N-acetyltransferase 1	chr8	NM_000662	9	108345	1	7
3022	SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	8
3023	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	1
3024	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	2
3025	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	3
3026	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	4
3027	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	5
3028	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	6
3029	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	7
3030	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	1
3031	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	2
3032	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	3
3033	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	4
3034	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	5
3035	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	6
3036	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	7
3037	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	8
3038	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	9
3039	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	10
3040	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	11
3041	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	12
3042	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	13
3043	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	14
3044	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	15
3045	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	1
3046	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	2
3047	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	3
3048	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	4
3049	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	5
3050	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	6
3051	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	7
3052	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	8
3053	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	9
3054	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	10
3055	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	11
3056	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	12

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

# SNP Information for IMS-JST105327

## General Information

JSNP ID : IMS-JST105327  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1324484	9	98923950

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	



3131	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	85
3132	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	86
3133	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	87
3134	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	88
3135	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	89
3136	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	90
3137	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	91
3138	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	92
3139	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	93
3140	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	94
3141	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	95
3142	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	96
3143	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	97
3144	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	98
3145	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	99
3146	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	100
3147	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	101
3148	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	102
3149	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	103
3150	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	104
3151	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	105
3152	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	106
3153	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	107
3154	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	108
3155	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	108
3156	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	109
3157	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	109
3158	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	110
3159	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	111
3160	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	112
3161	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	113
3162	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	114
3163	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	115
3164	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	116
3165	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	117
3166	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463
3167	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463



3168	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	3
3169	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	4
3170	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	4
3171	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	5
3172	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	6
3173	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	7
3174	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	8
3175	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	9
3176	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	10
3177	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	11
3178	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	12
3179	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	13
3180	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	14
3181	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	15
3182	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	16
3183	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	17
3184	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	18
3185	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	19
3186	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	20
3187	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	21
3188	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	22
3189	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	23
3190	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	24
3191	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	25
3192	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	26
3193	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	27
3194	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	28
3195	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	29
3196	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	30
3198	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	31
3199	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	32
3200	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	33
3201	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	34
3202	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	35
3203	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	36
3204	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	37
3205	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	38

3206	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	39
3207	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	40
3208	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	41
3209	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	42
3210	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	43
3211	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	44
3212	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	45
3213	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	46
3214	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	47
3215	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	48
3216	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	49
3217	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	50
3218	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	51
3219	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	52
3220	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	53
3221	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	54
3222	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	55
3223	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	56
3224	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	57
3225	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	58
3226	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	59
3227	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	60
3228	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	61
3229	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	62
3230	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	63
3231	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	64
3232	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	65
3233	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	66
3234	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	67
3235	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	68
3236	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	1
3237	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	2
3238	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	3
3239	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	4
3240	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	5
3241	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	6
3242	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	7





3316	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	78
3317	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	79
3318	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	80
3319	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	81
3320	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	82
3321	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	83
3322	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	84
3323	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	85
3324	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	86
3325	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	87
3326	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	88
3327	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	89
3328	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	90
3329	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	91
3330	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	92
3331	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	93
3332	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	94
3333	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	95
3334	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	96
3335	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	97
3336	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	98
3337	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	99
3338	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	100
3339	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	101
3340	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	102
3341	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	103
3342	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	104
3343	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	105
3344	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	106
3345	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	107
3346	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	108
3347	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	109
3348	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	110
3349	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	111
3350	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	112
3351	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	113
3352	CYP3A4	cytochrome P450, subfamily 11A, polypeptide 4	chr7	NM_017460	1576	124010	13	1

Table 6.6.6.6

3353	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	2
3354	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	3
3355	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	4
3356	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	4
3357	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	5
3358	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	6
3359	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	7
3360	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	8



Fig. 144 B

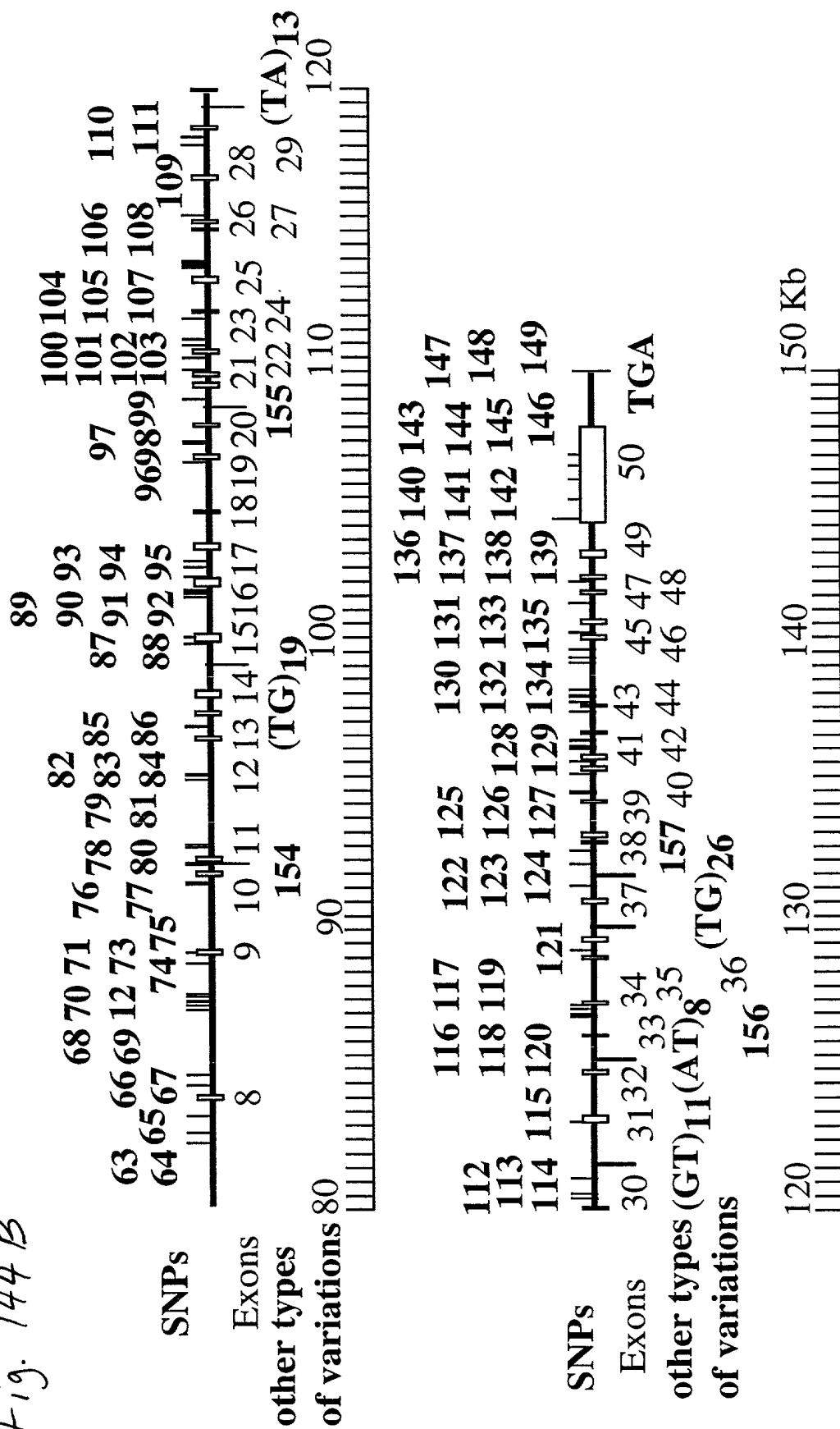




Fig. 145 ATP binding cassette, subfamily A, member 4 (ABCA4)

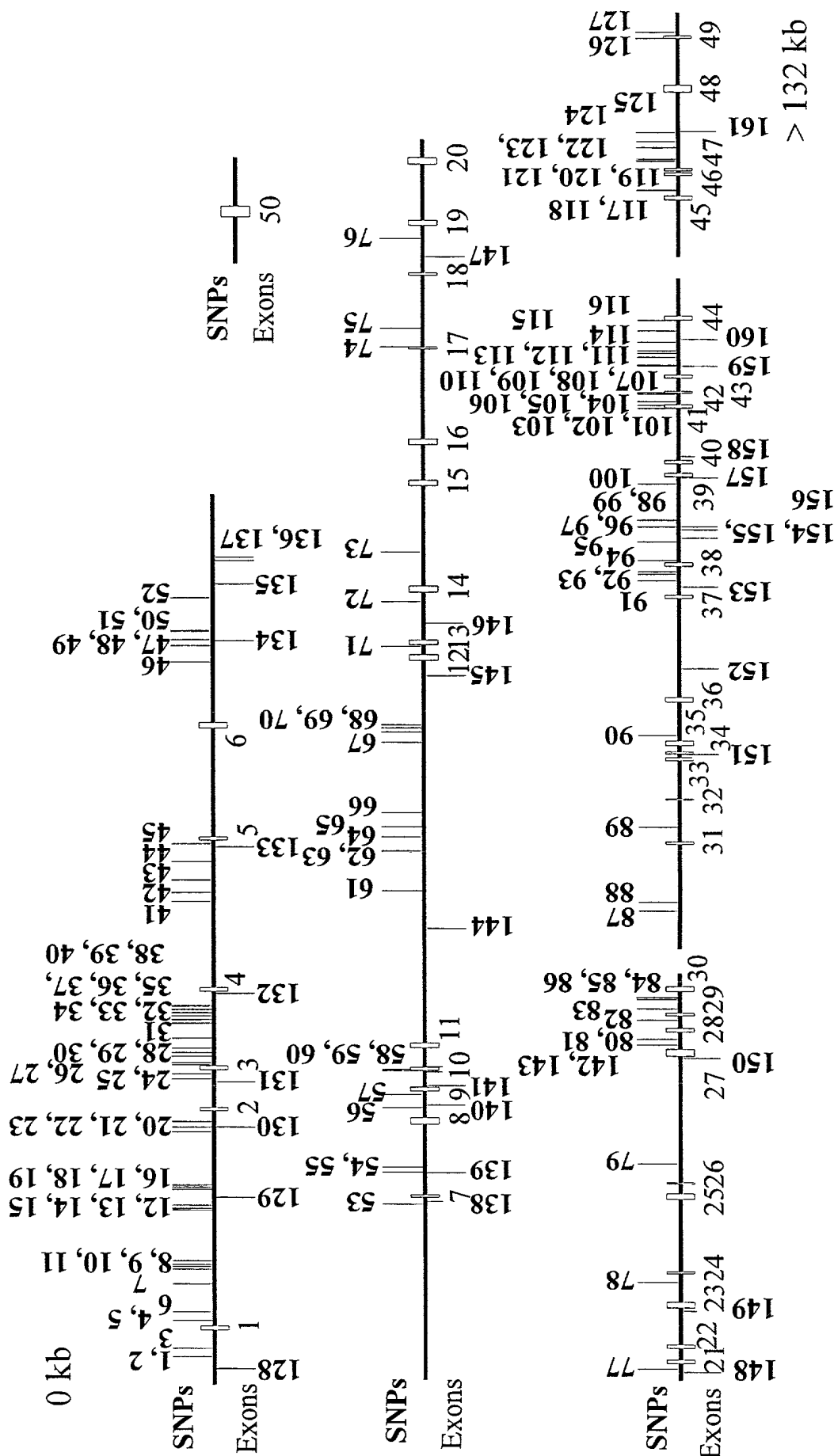


Fig. 146

# ATP binding cassette subfamily A, member 7 (ABCA7)

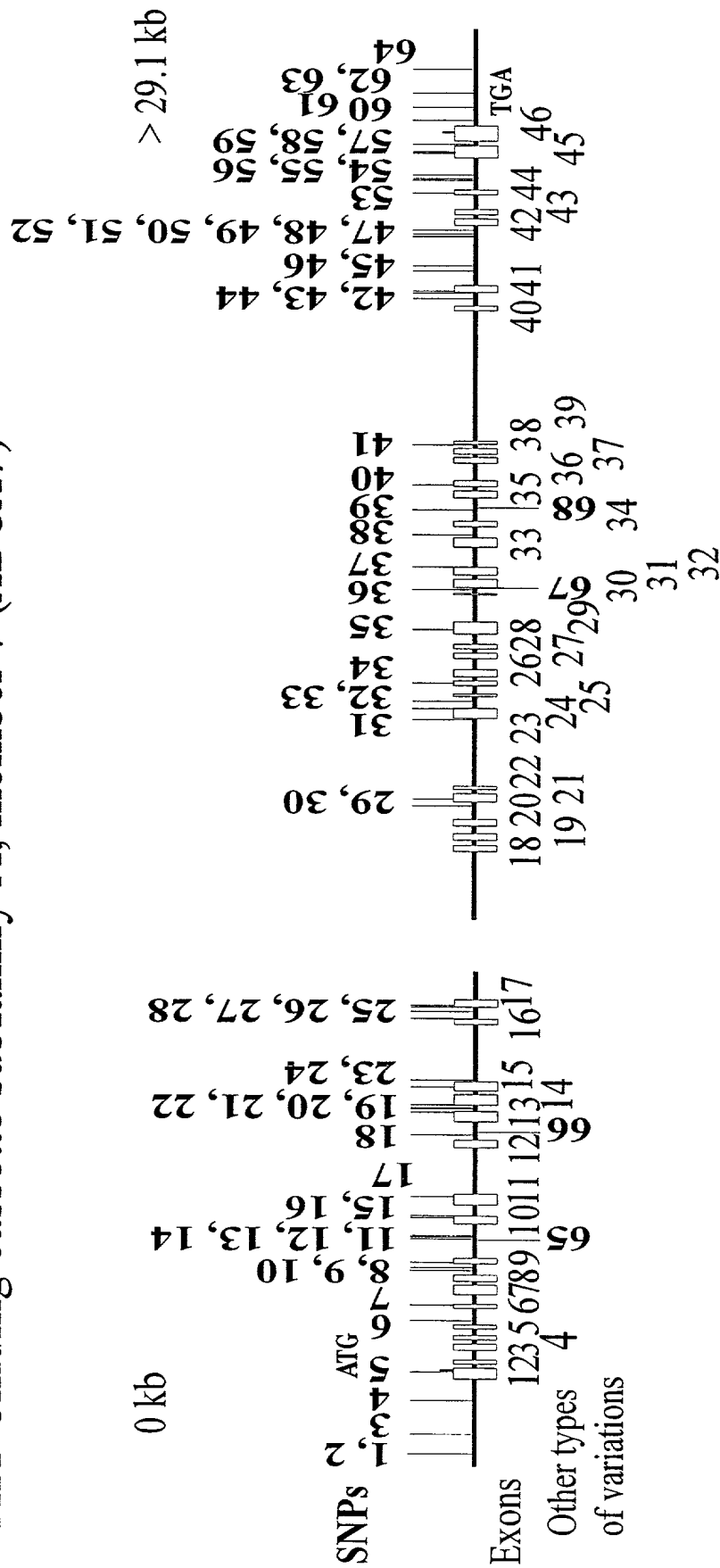


Fig. 147

ATP binding cassette transporter subfamily A member 8 (ABCA8)

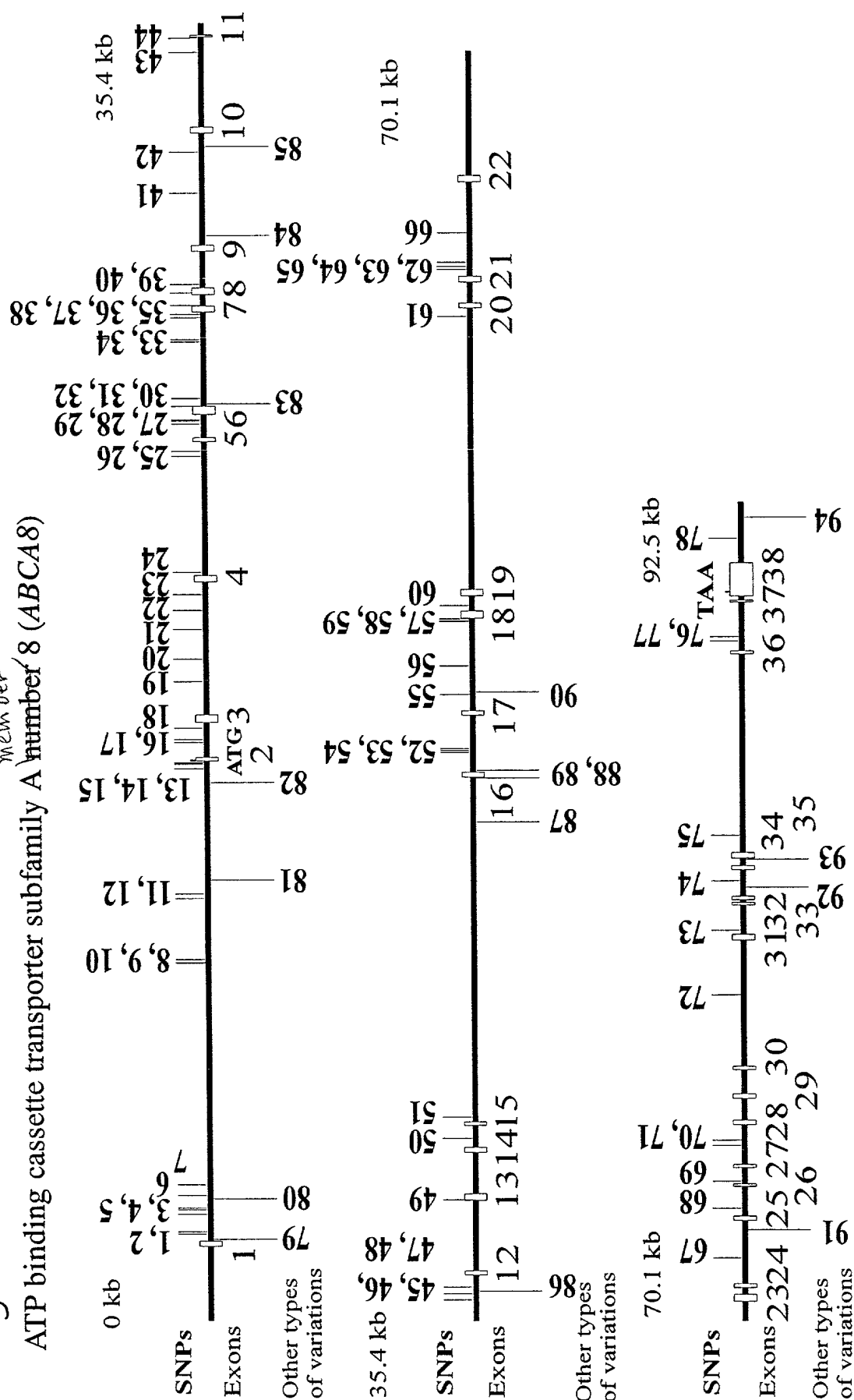


Fig. 148

*ATP-binding cassette, sub-family B, member1 (ABCB1)*

ACCESSION AC002457.1  
AC005068.1

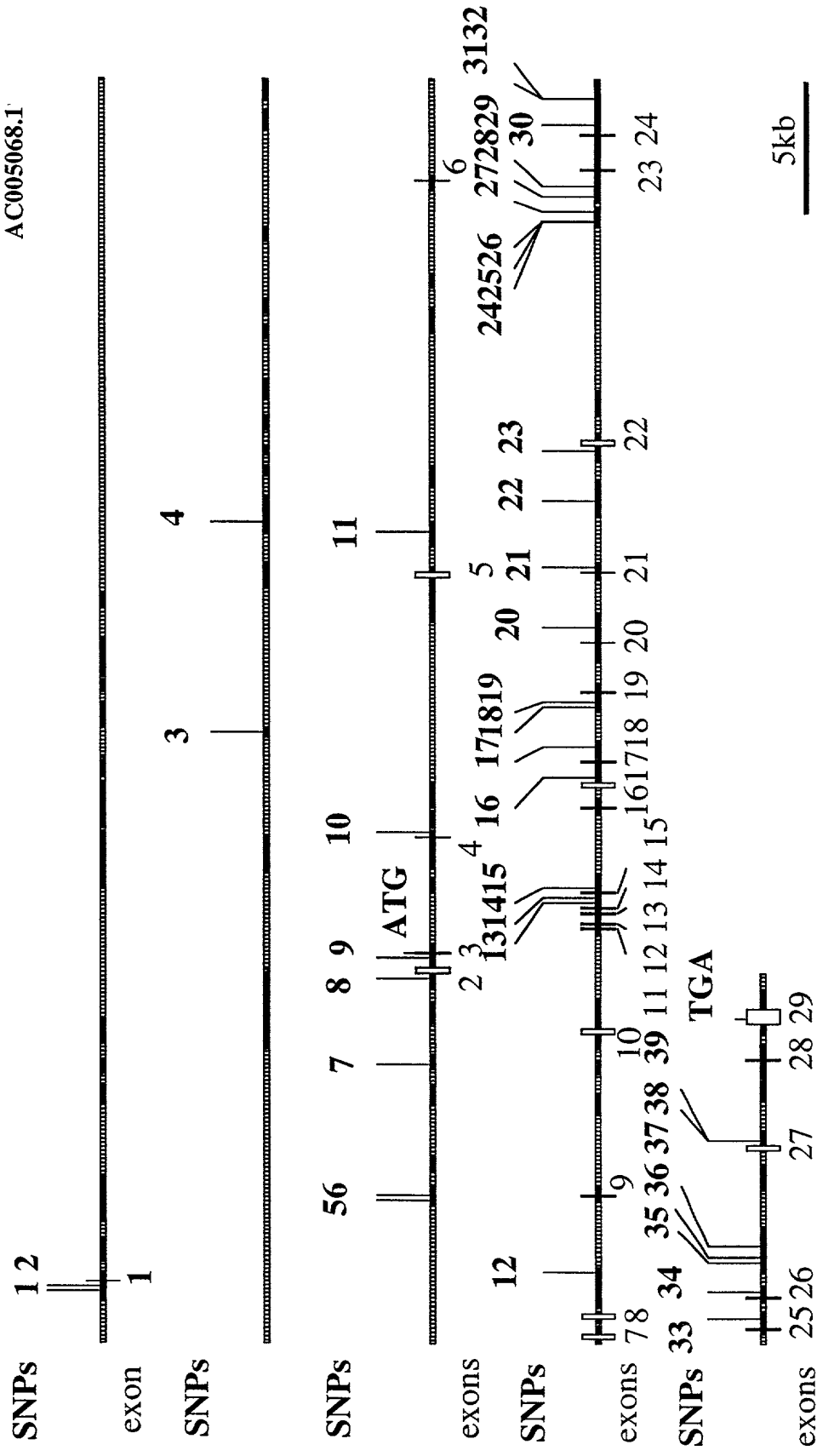


Fig. 149 ATP-binding cassette, sub-family B, member 4 (ABCB4)

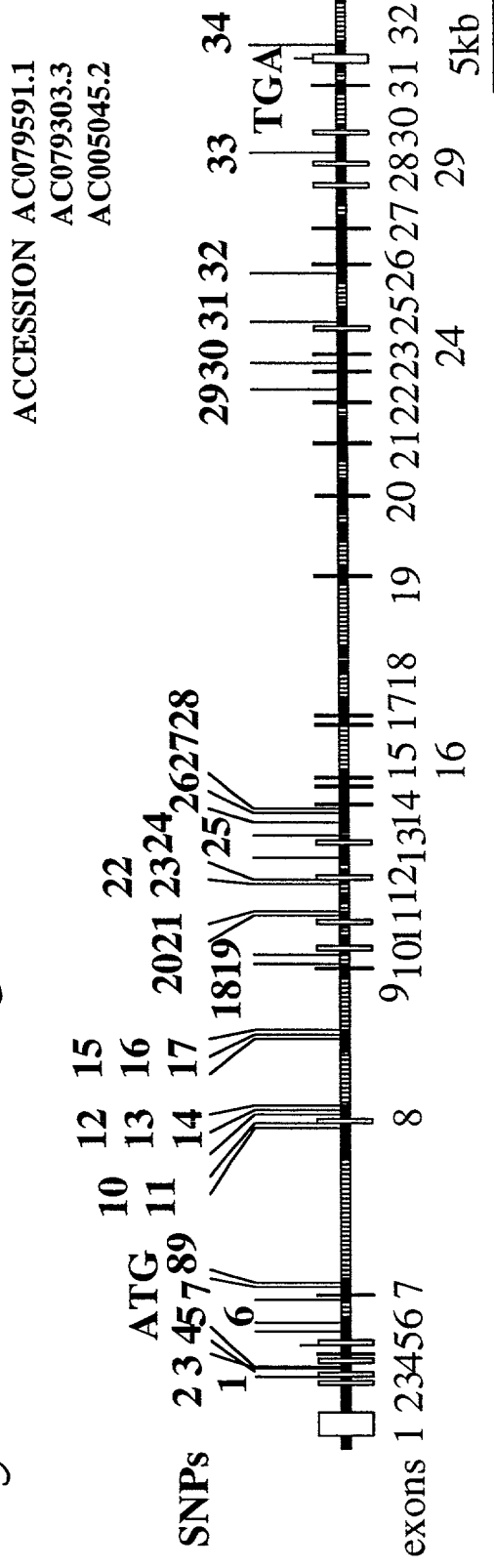


Fig. 150 ATP-binding cassette, sub-family B, member 7 (ABCB7)

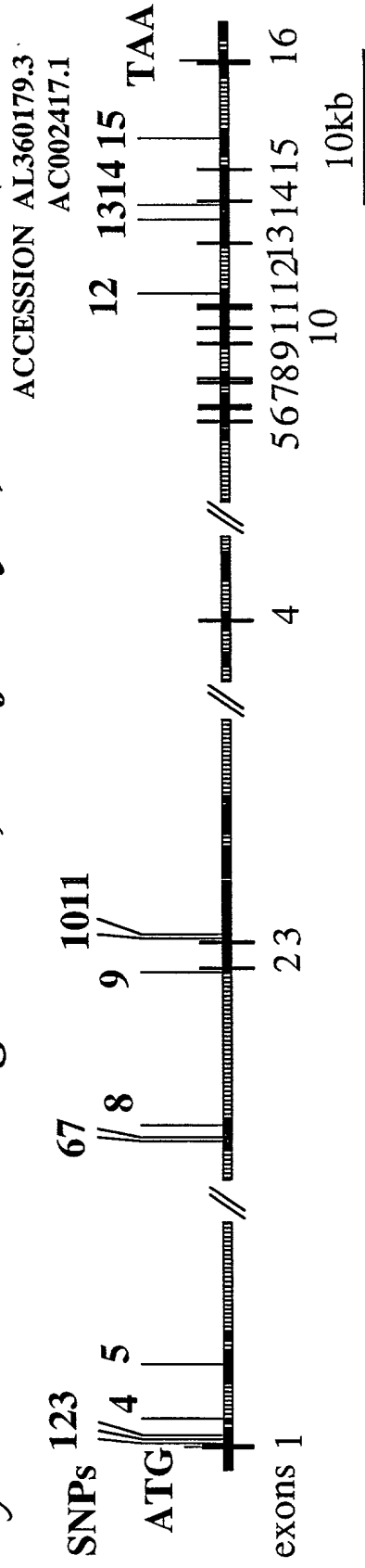


Fig. 151

ATP-binding cassette, sub-family B, member 8 (ABCB8)

ACCESSION AC010973.4

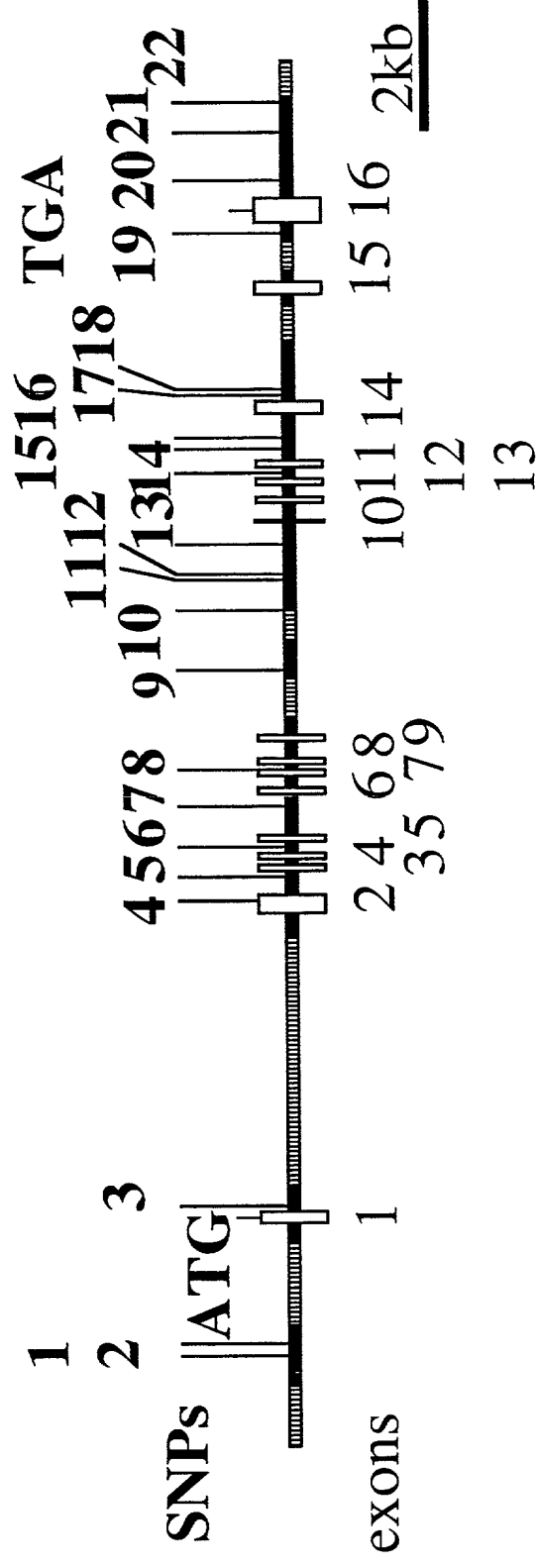


Fig. 152

***ATP binding cassette, sub-family B, member 9  
(ABCB9)***

ACCESSION AC026362.9  
AC073857.10

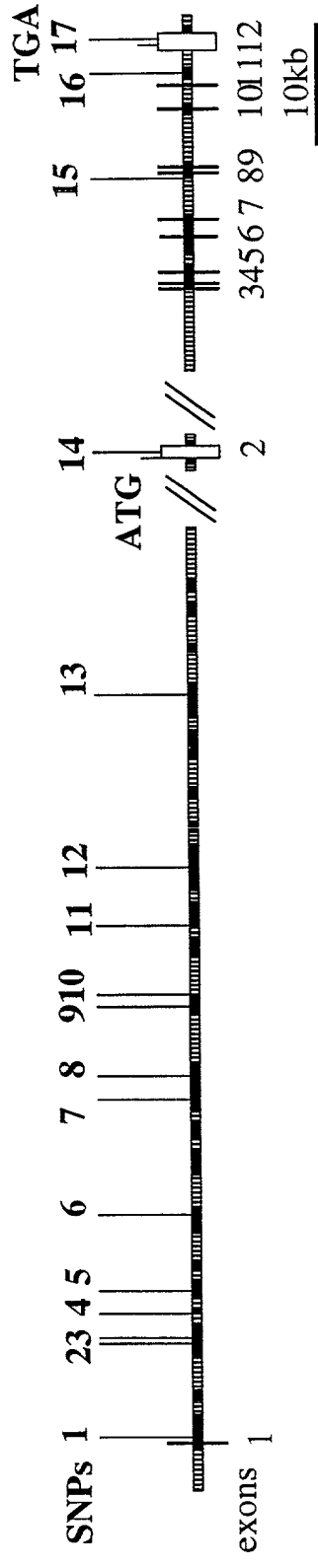


Fig. 153

***ATP binding cassette, sub-family B, member 10  
(ABCB10)***

ACCESSION AL121990.9

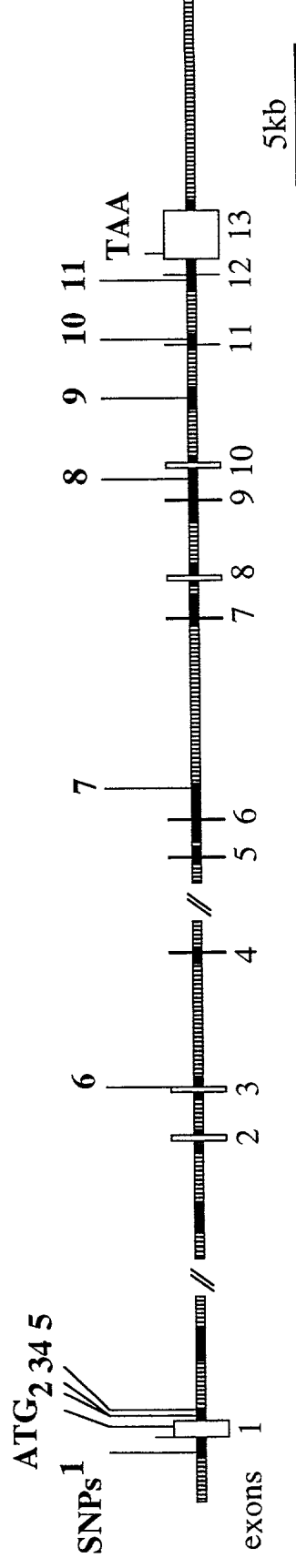


Fig. 254 NADH ubiquinone oxidoreductase 1 alpha subcomplex 1 (*NDUF41*)

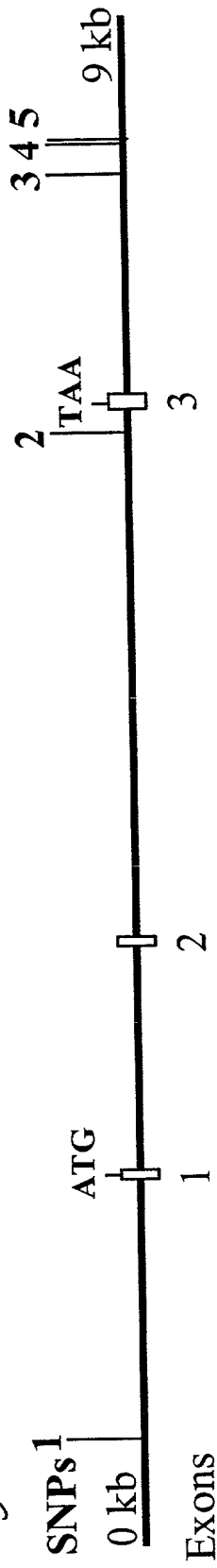


Fig. 255 NADH ubiquinone oxidoreductase 1 alpha subcomplex 2 (*NDUF42*)

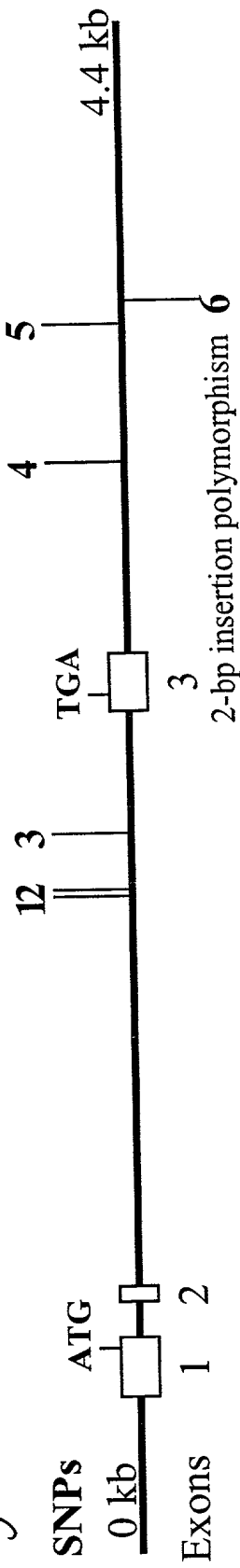


Fig. 256 NADH ubiquinone oxidoreductase 1 alpha subcomplex 3 (*NDUF43*)

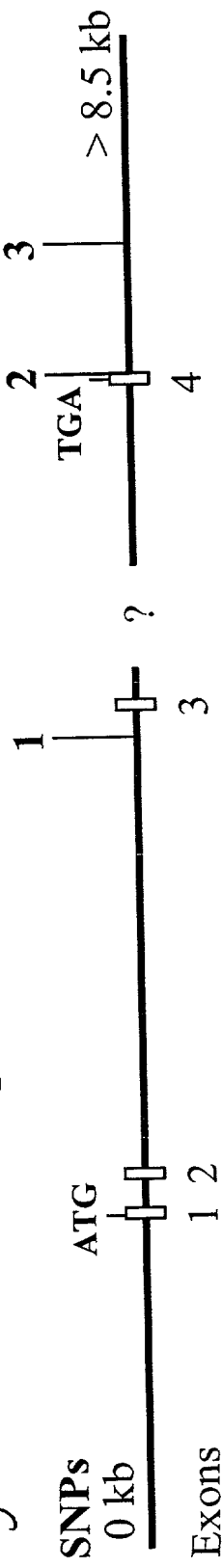




Fig. 155

# *ATP-binding cassette, sub-family C (CFTR/MRP), member 1*

(ABCC1)

ACCESSION AC026452.5  
AC025778.4

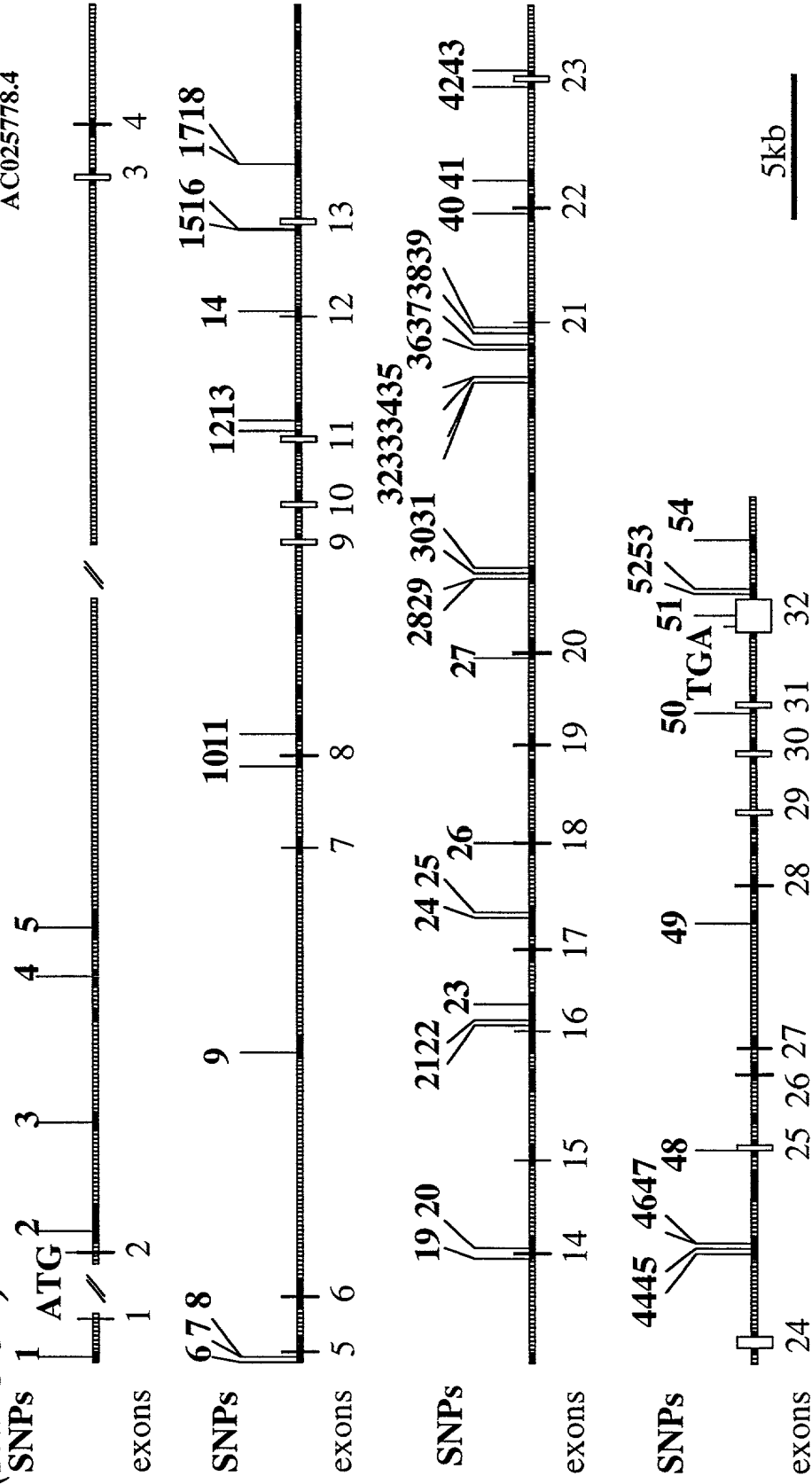


Fig. 156

# *ATP-binding cassette, sub-family C, member2 (ABCC2)*

ACCESSION AL392107.4

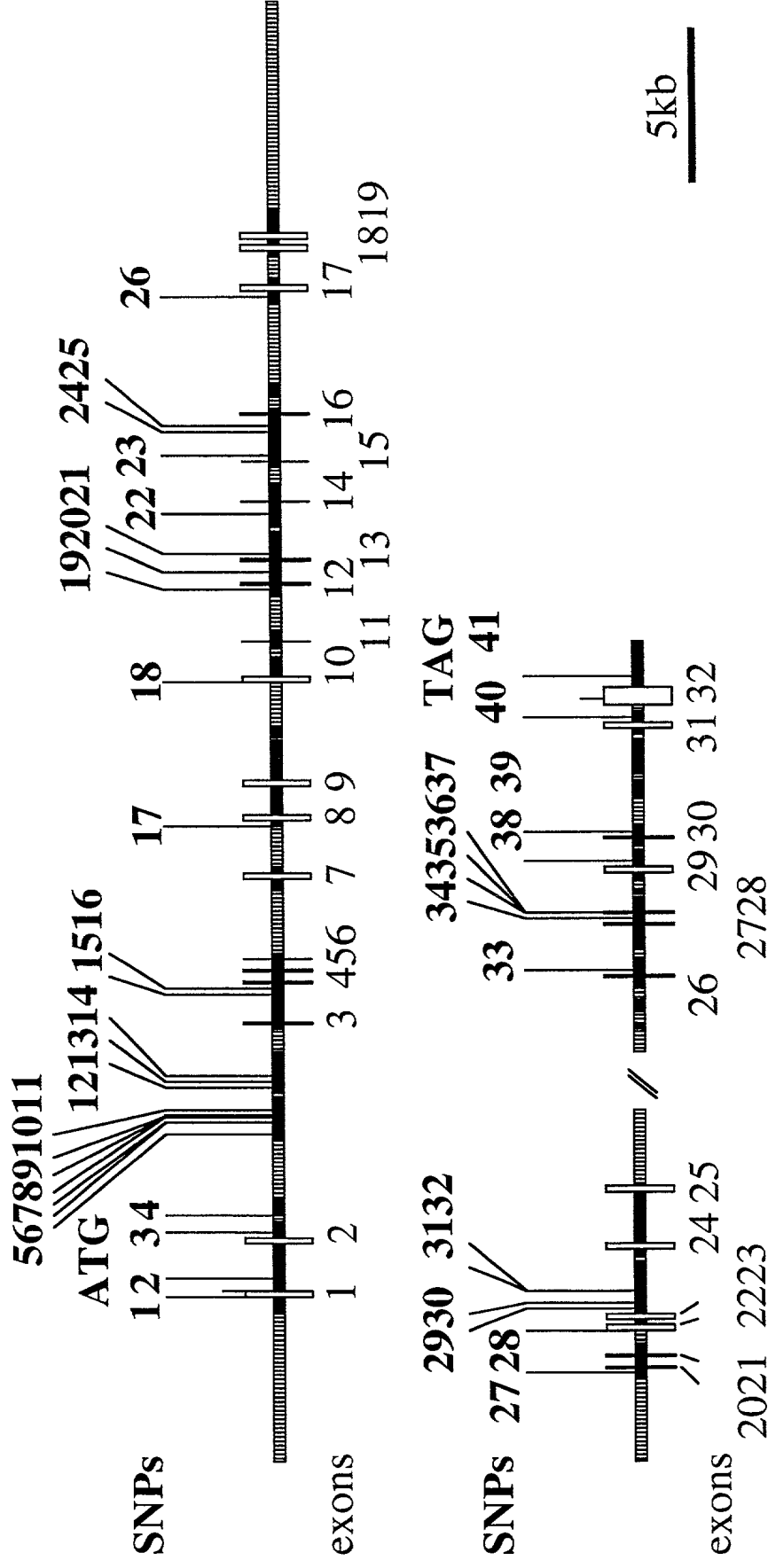


Fig. 157

***ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3)***

**ACCESSION** AC004590.1  
AC005921.3

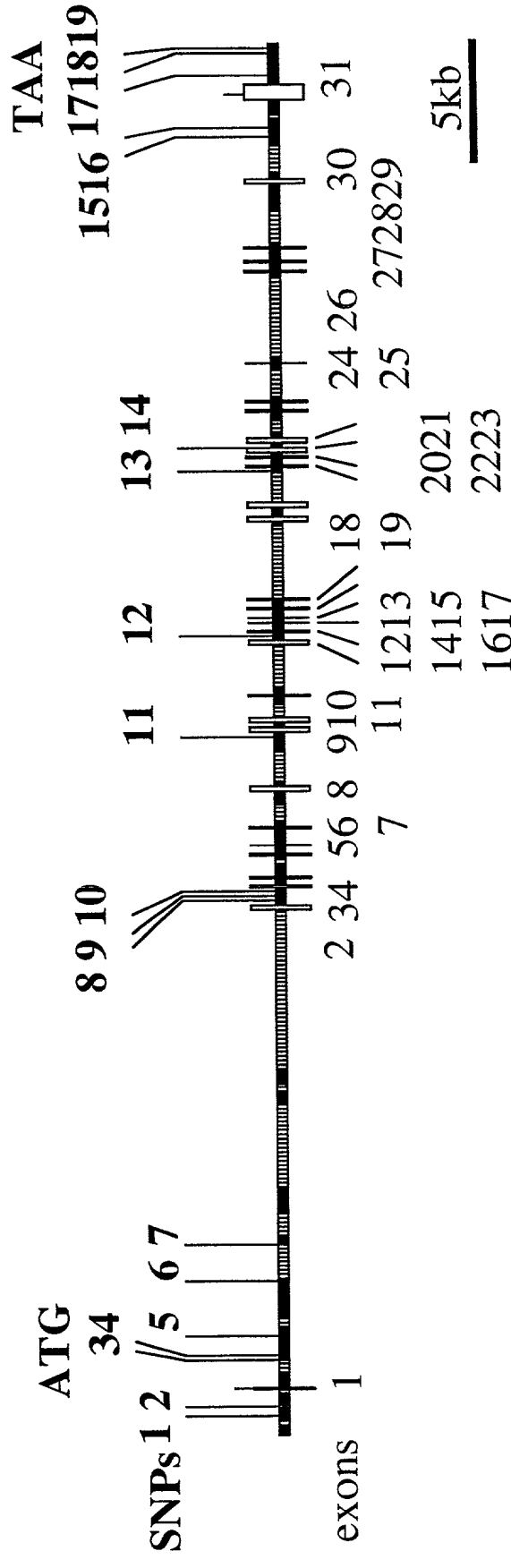


Fig. 158A *ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4)*

ACCESSION AL356257.11 AL157818.12 AL139381.12

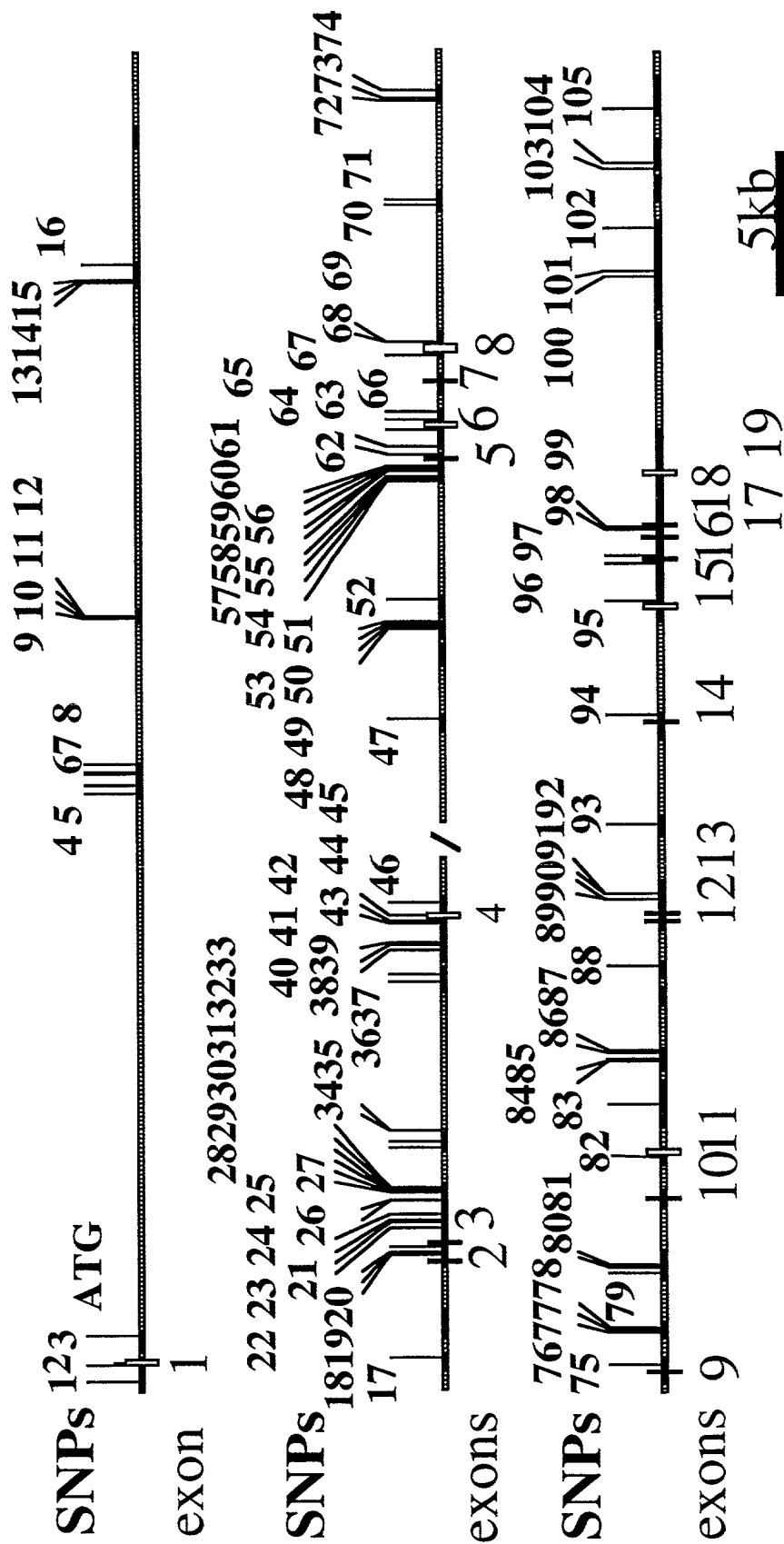


Fig. 158B

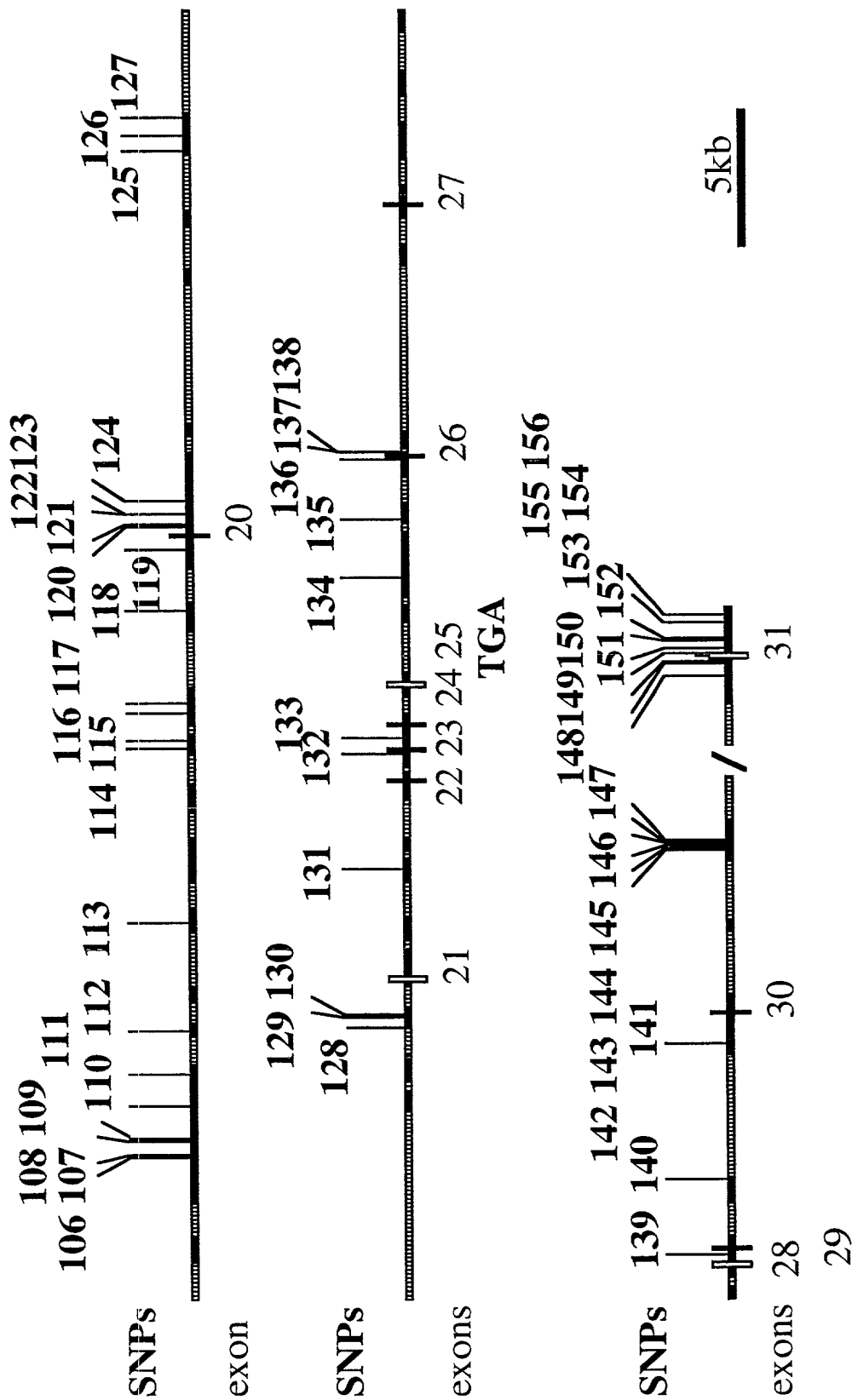


Fig. 159 ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)

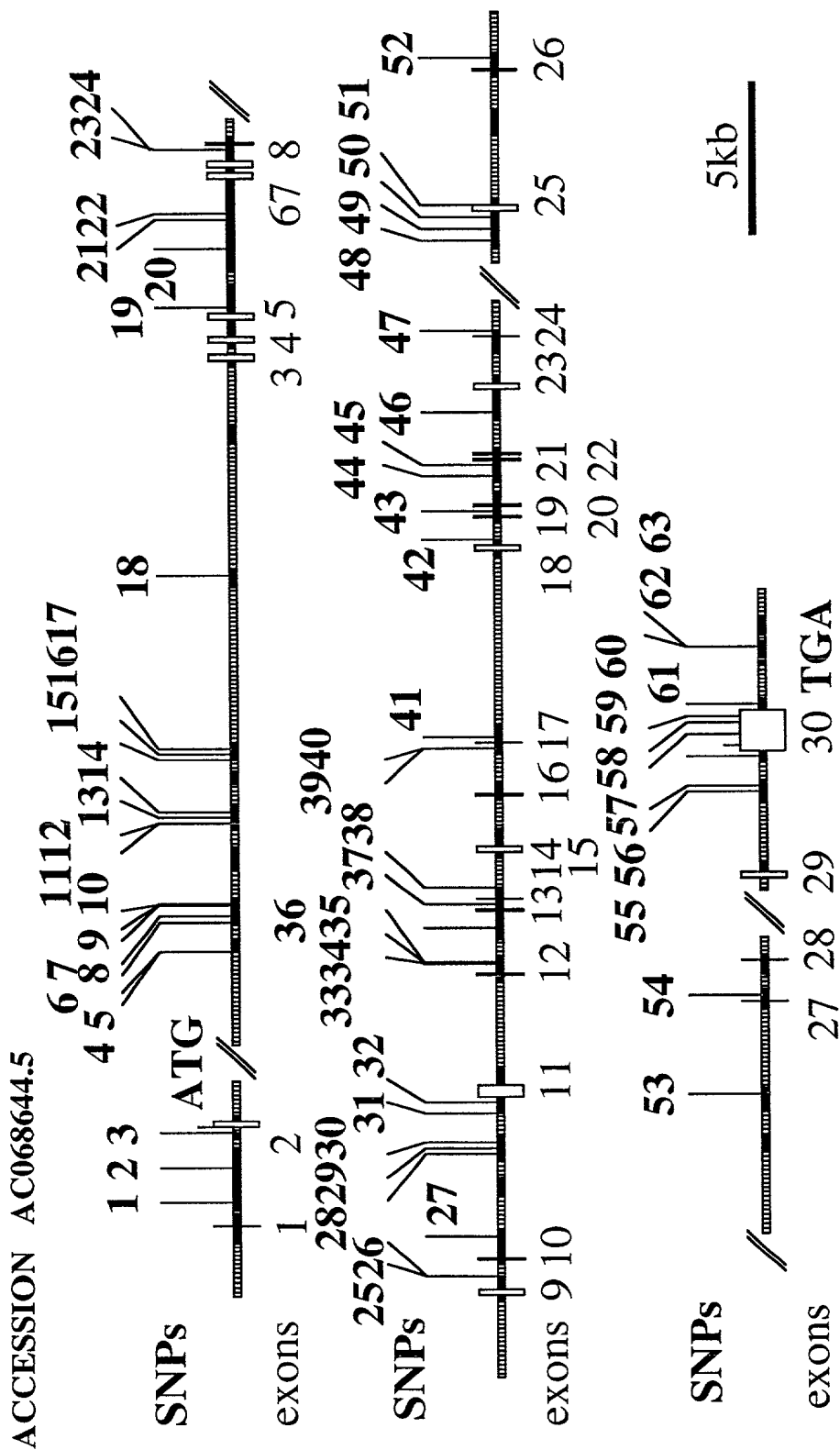


Fig. 160 ATP binding cassette, sub-family C (CFTR/MRP), member 7 (ABCC7)

ACCESSION AC000111.1 AC000061.1

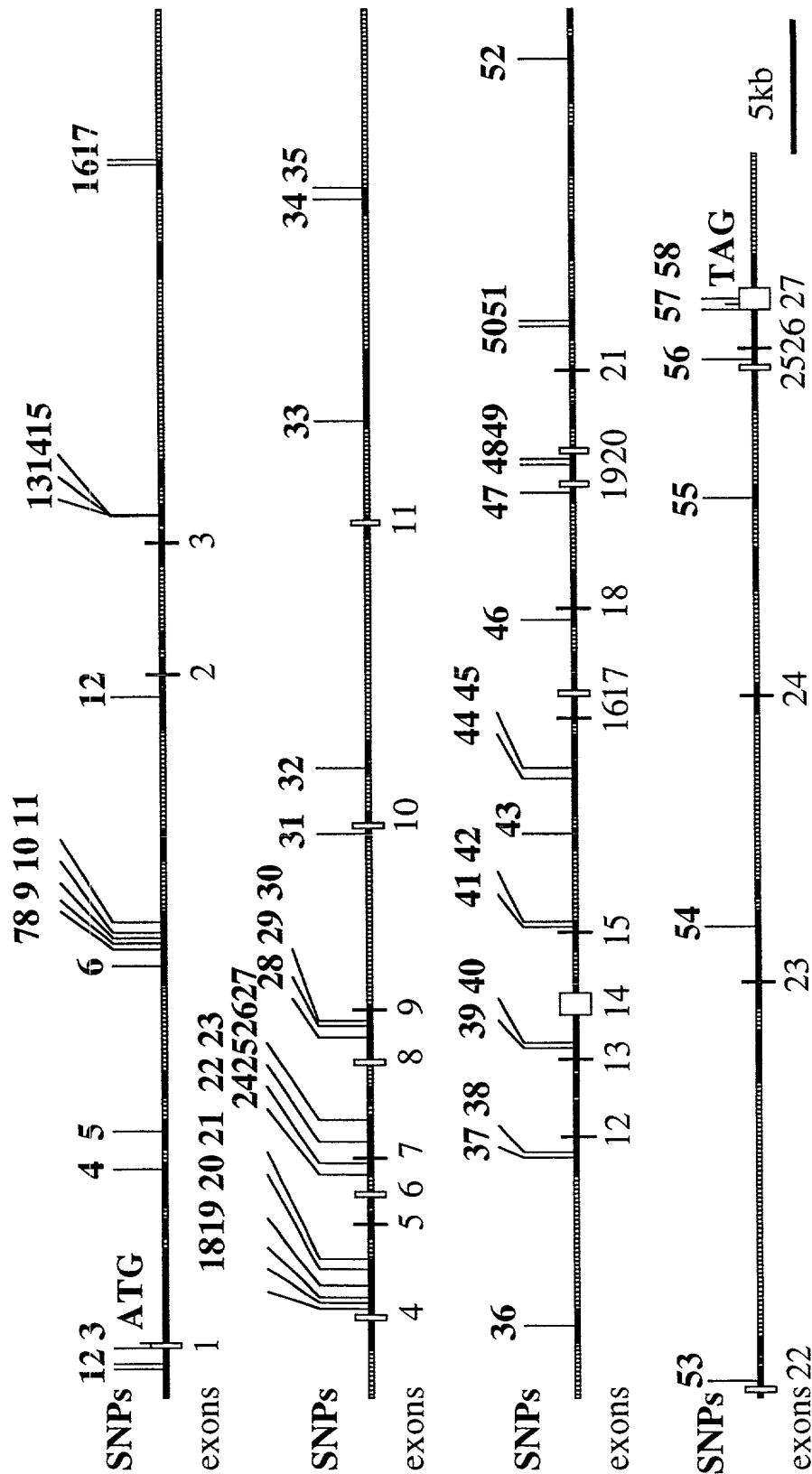
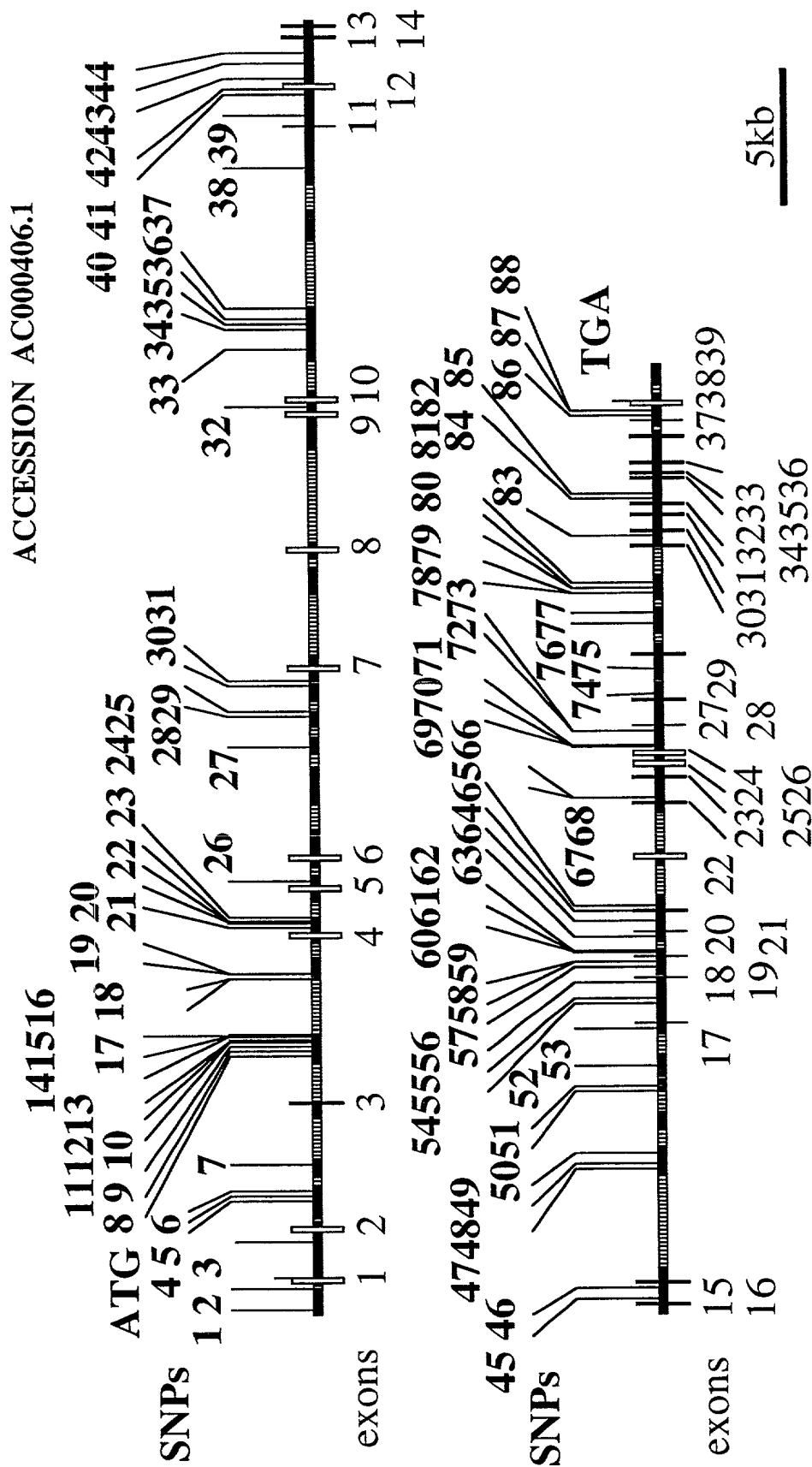


Fig. 161 ATP binding cassette, sub-family C (CFTR/MRP), member 8 (ABCC8)





**Fig. 162** *ATP binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9)*

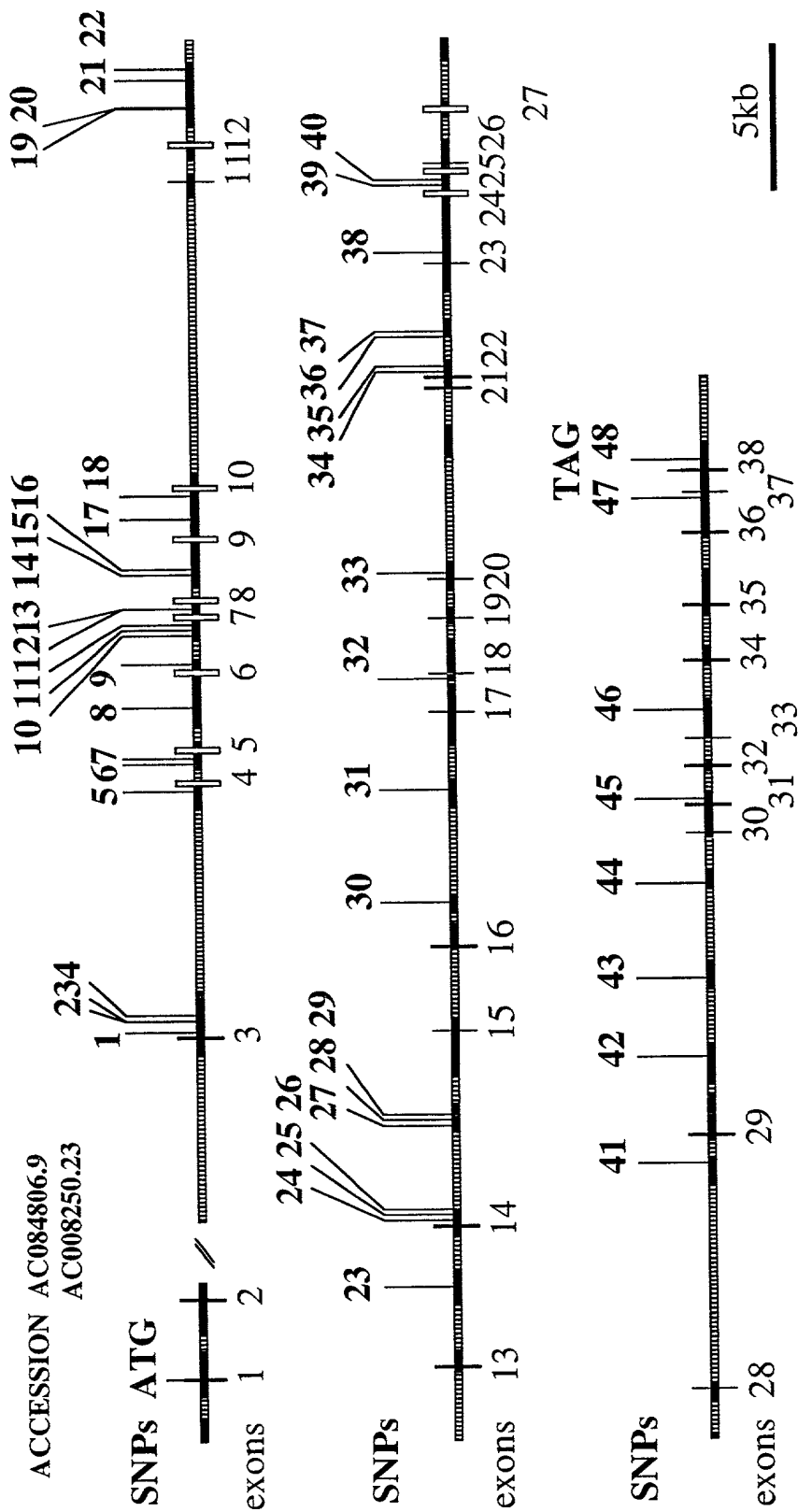


Fig. 163

ATP binding cassette subfamily D, member 1 (*ABCD1*)

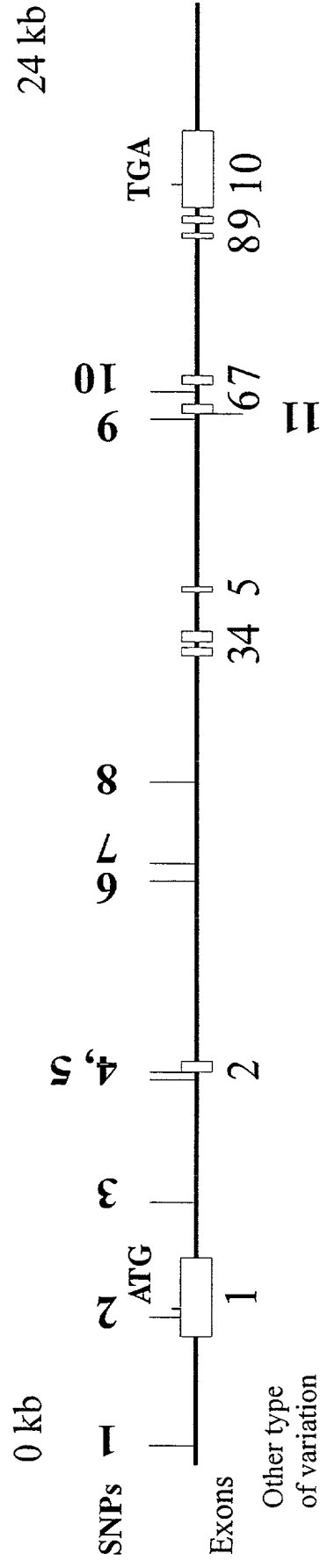




Fig. 165

ATP binding cassette subfamily D, member 4 (*ABCD4*)

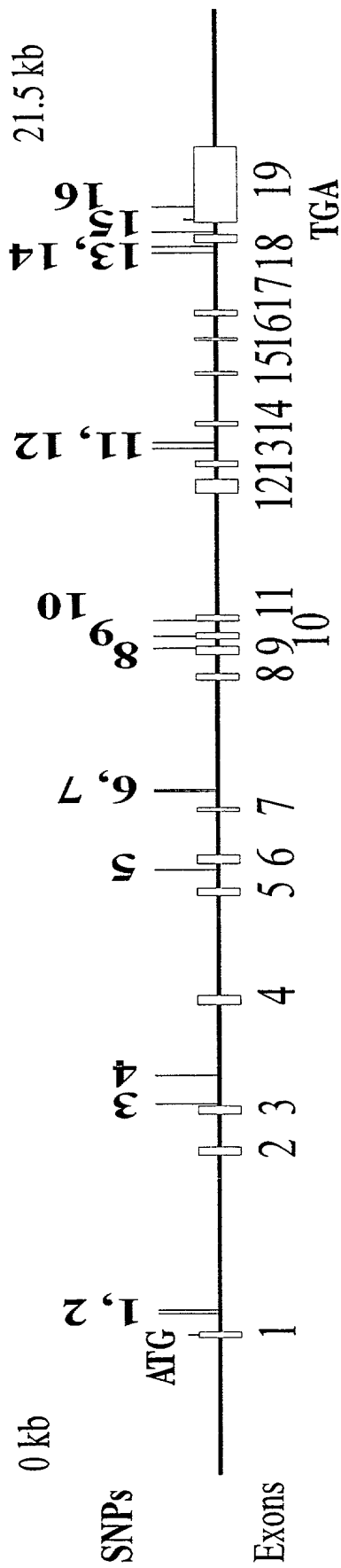


Fig. 166

ATP binding cassette subfamily G, member 1 (*ABCG1*)

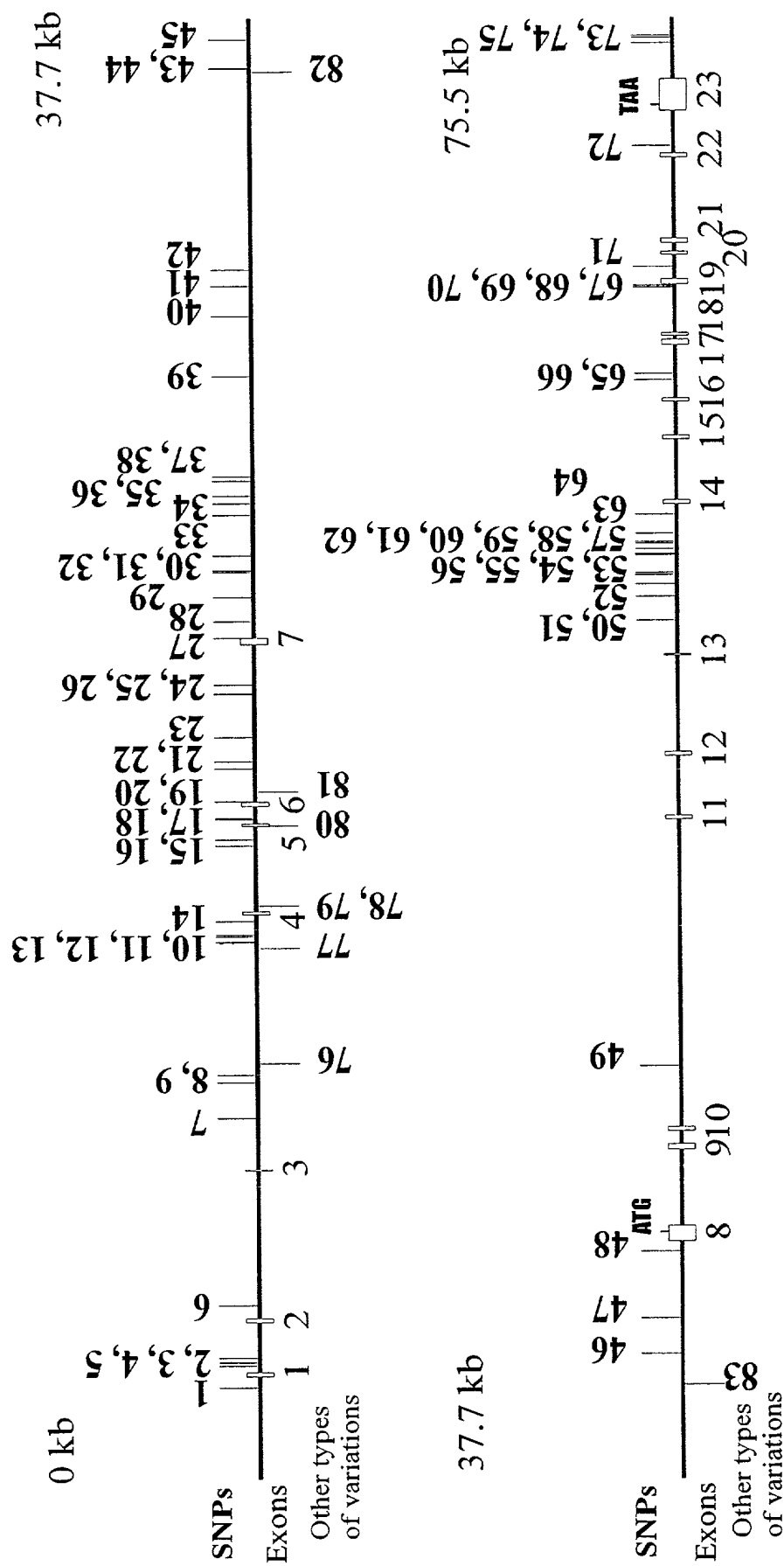


Fig. 167

# ATP binding cassette subfamily G, member 2 (ABCG2)

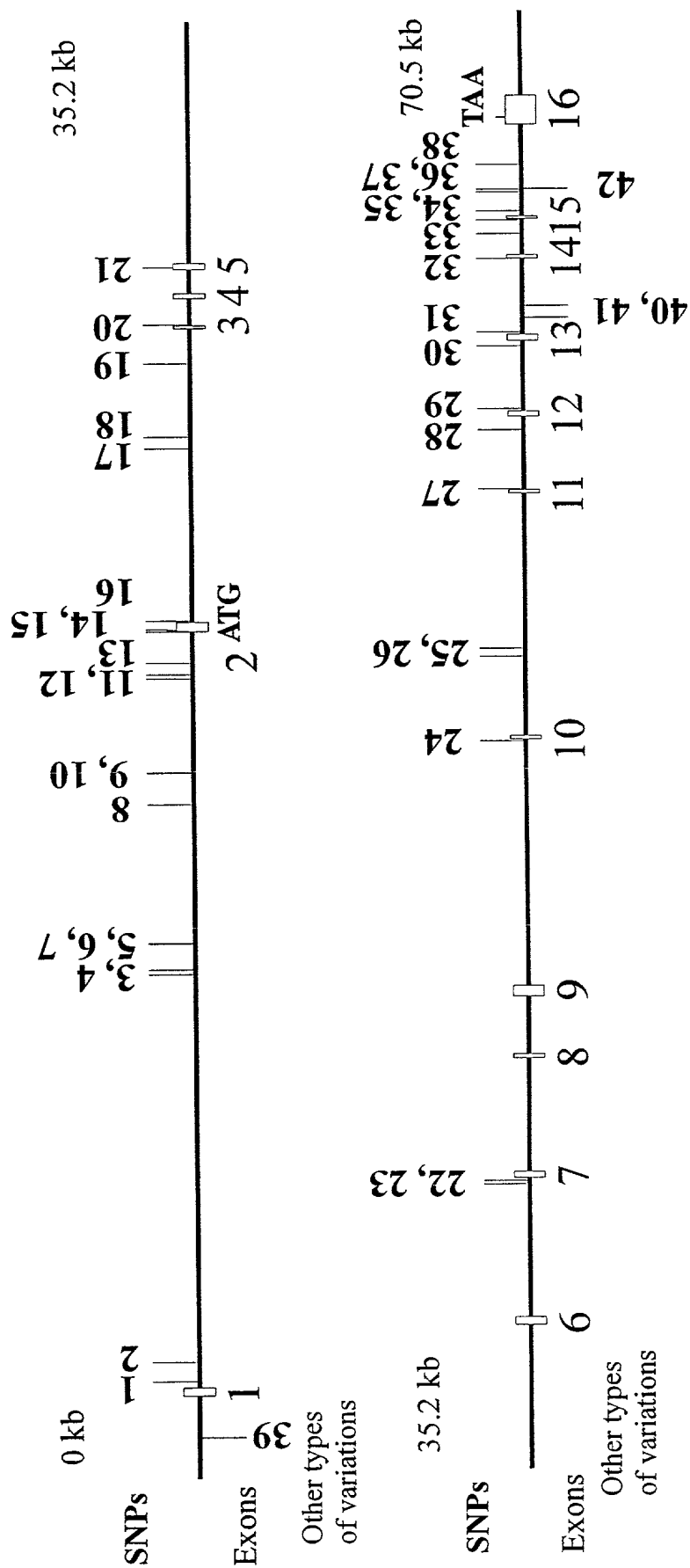




Fig. 169

ATP binding cassette transporter subfamily G number 5 (ABCG5)

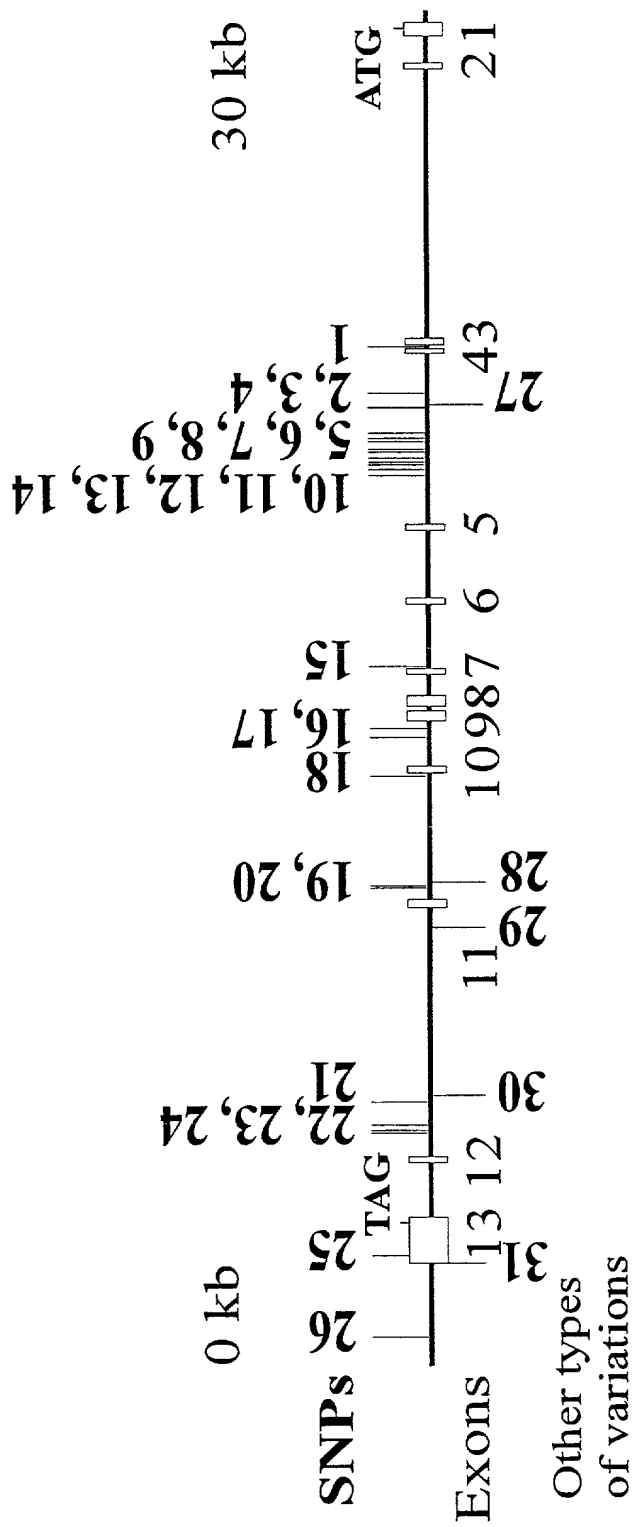




Fig. 170

ATP binding cassette transporter subfamily G number 8 (ABCG8)

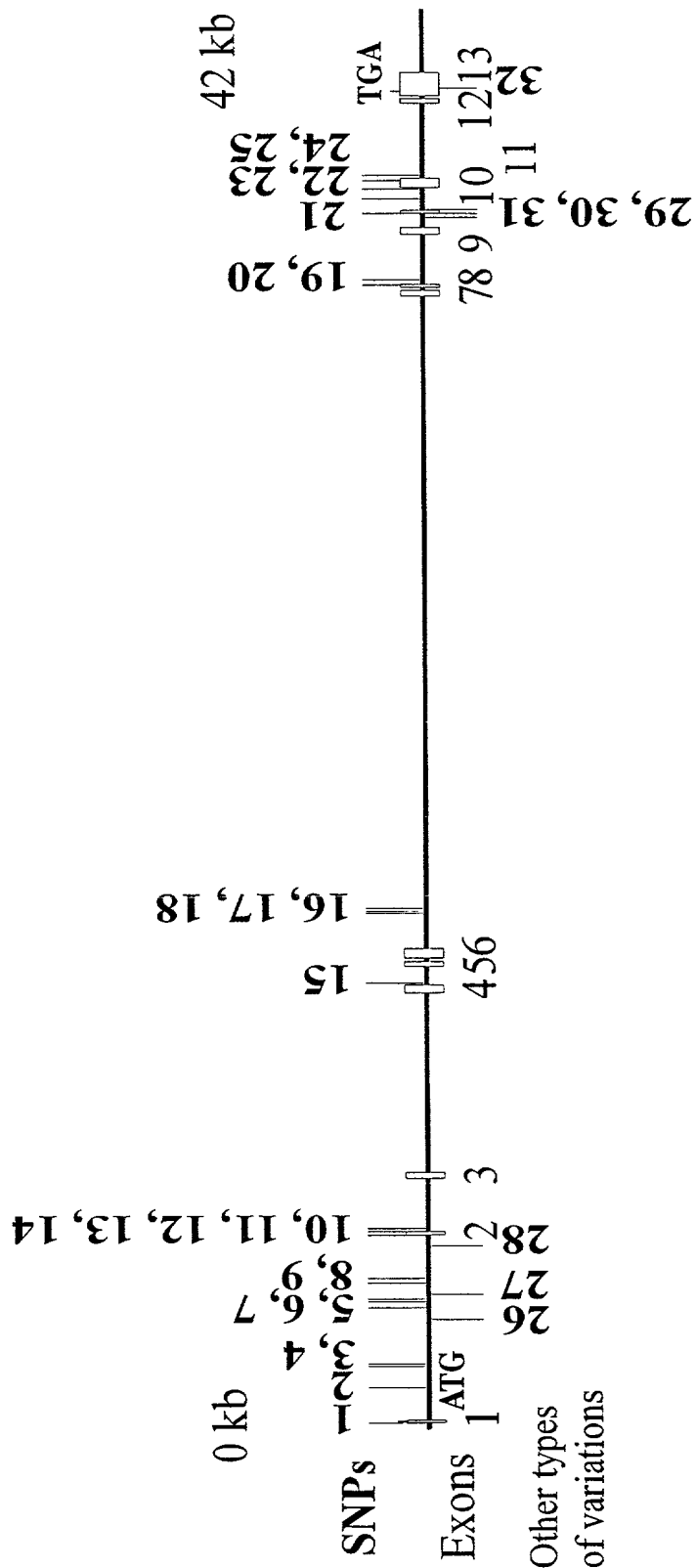


Fig. 171

ATP binding cassette subfamily E, member 1 (*ABCE1*)

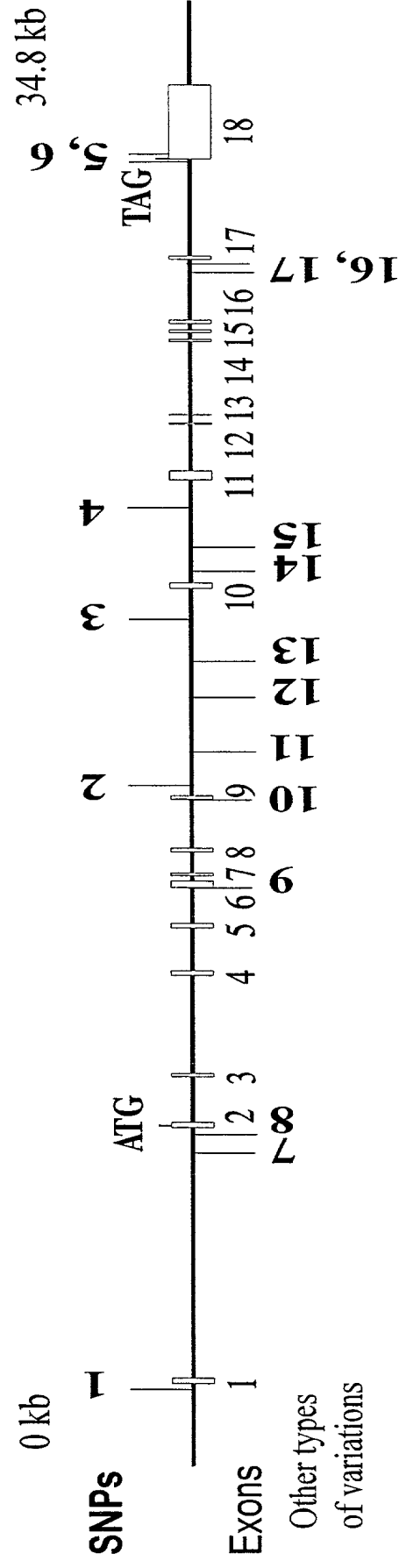


Fig. 172  
ATP binding cassette superfamily F member 1 (ABCF1)

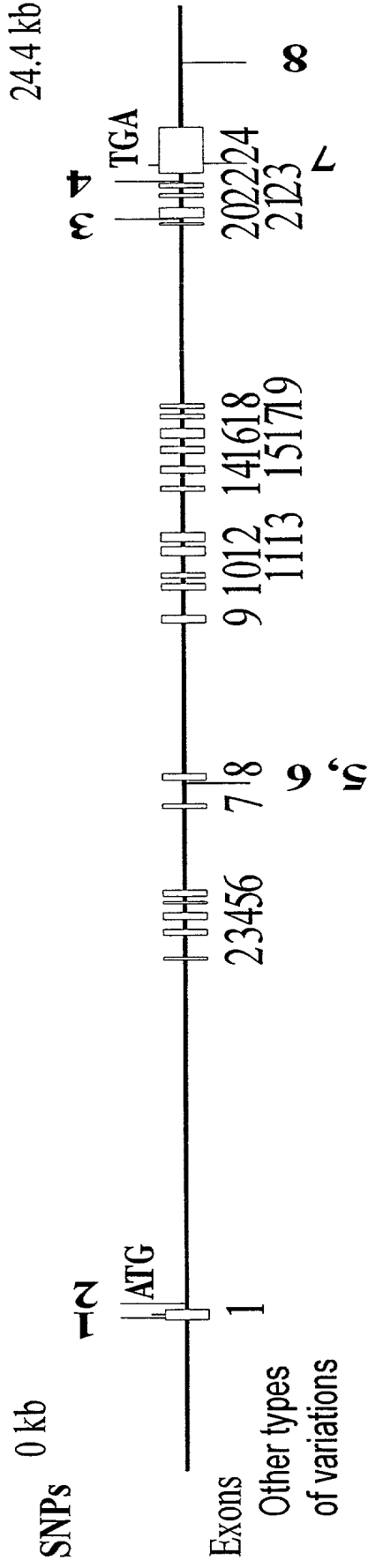


Fig. 173

Human organic anion transporter 1 (*hOAT1*)

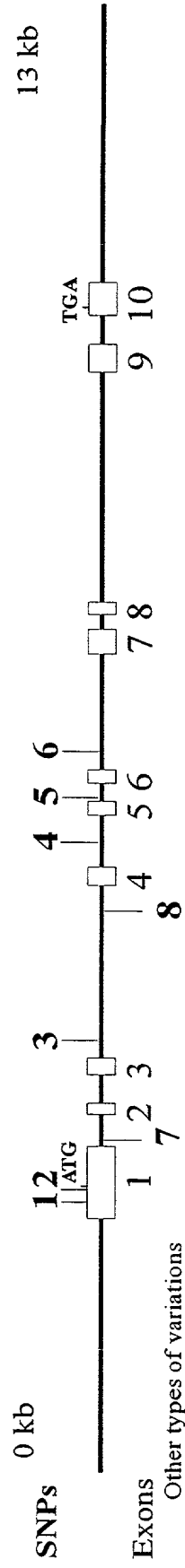


Fig. 174

Human organic anion transporter 2 (*hOAT2*)

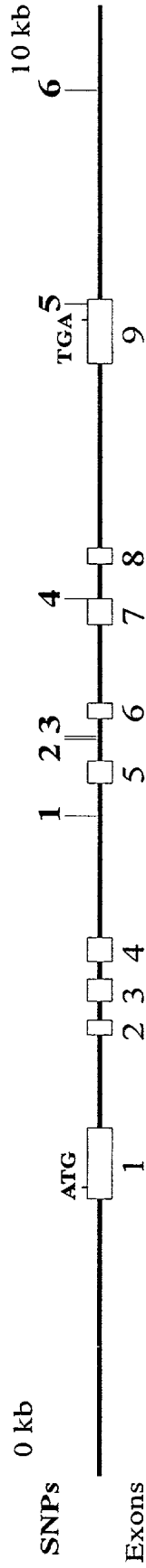


Fig. 175

Human organic anion transporter 3 (*hOAT3*)



Fig. 176

# Human organic anion transporting polypeptide 1 (*hOATP1*)

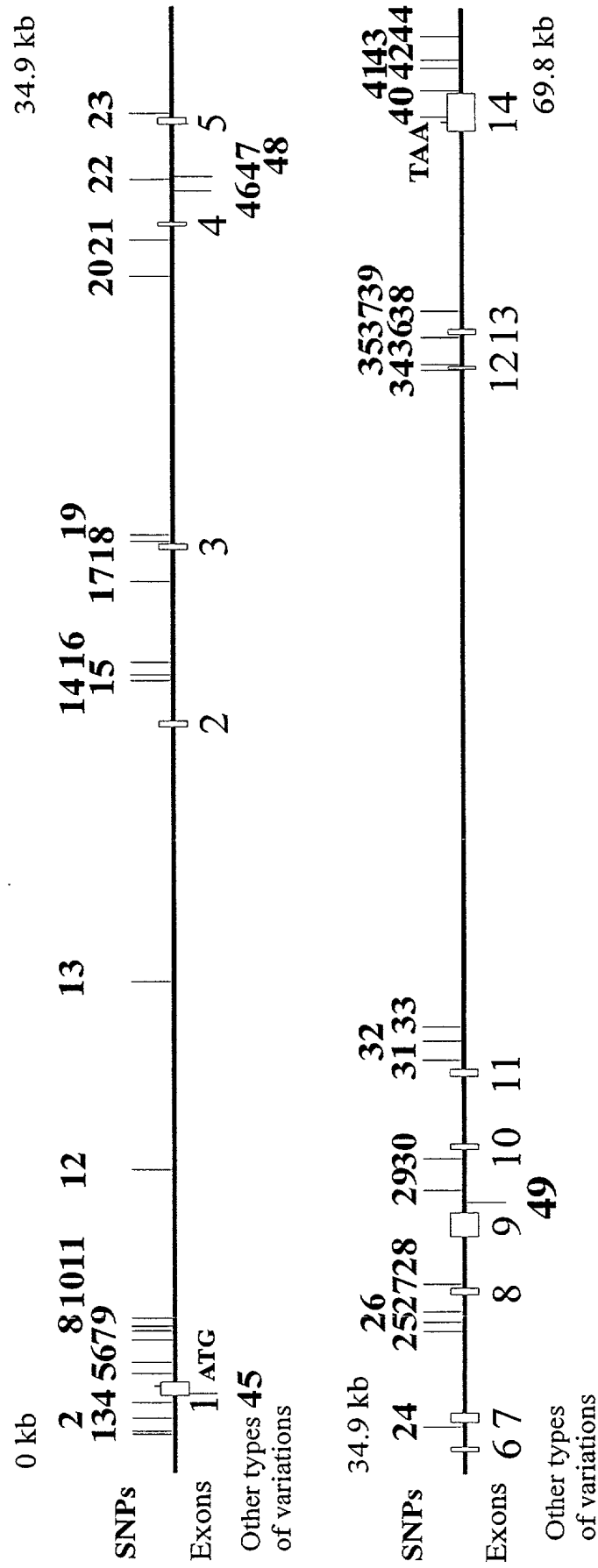


Fig. 177

# Human organic anion transporting polypeptide 2 (*hOATP2*)

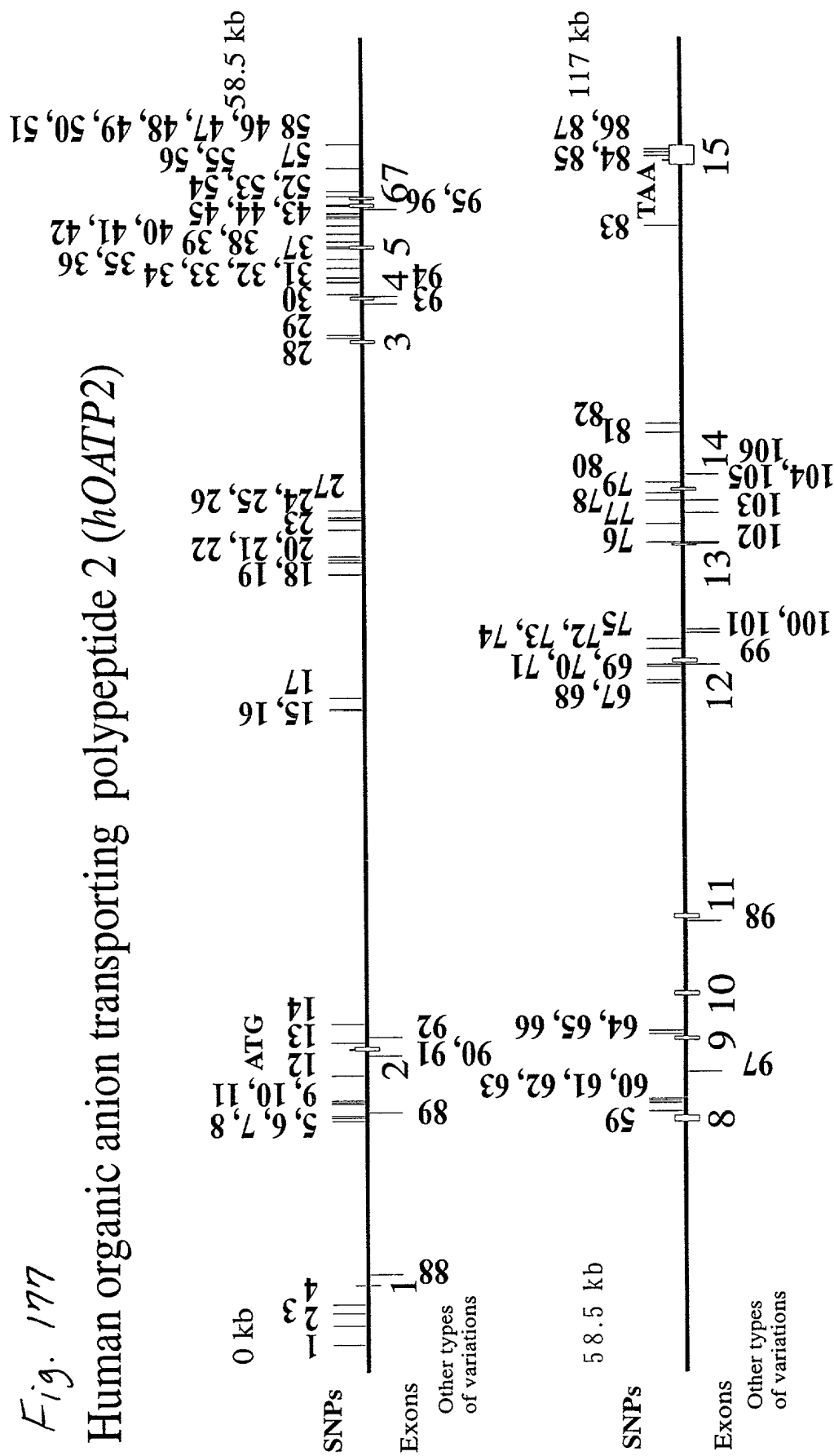


Fig. 178

Human organic anion transporting polypeptide 8 (*hOATP8*)

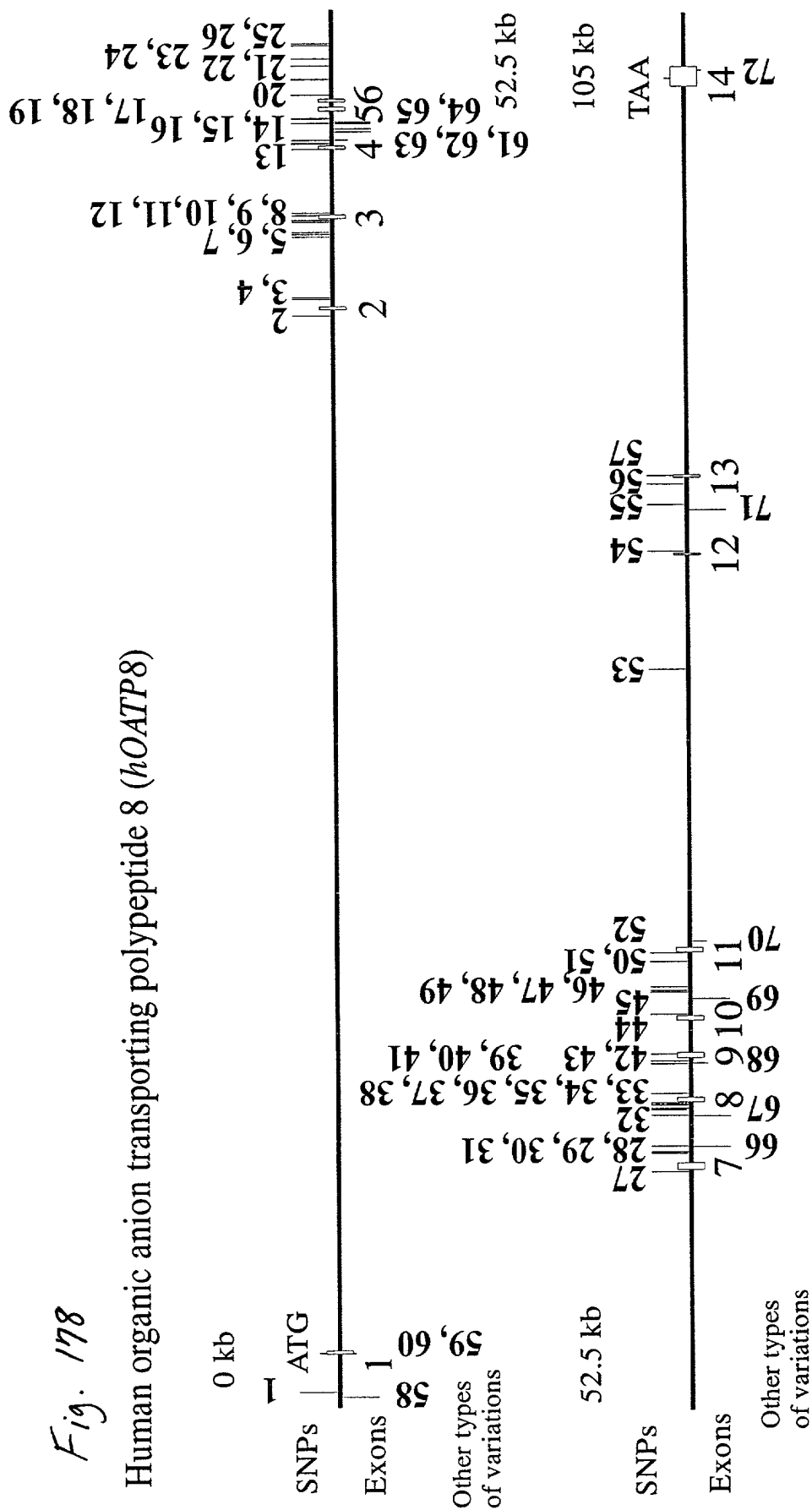


Fig. 179 *Transporter associated with antigen processing 1 (TAP1)*  
 ACCESSION X66401.1

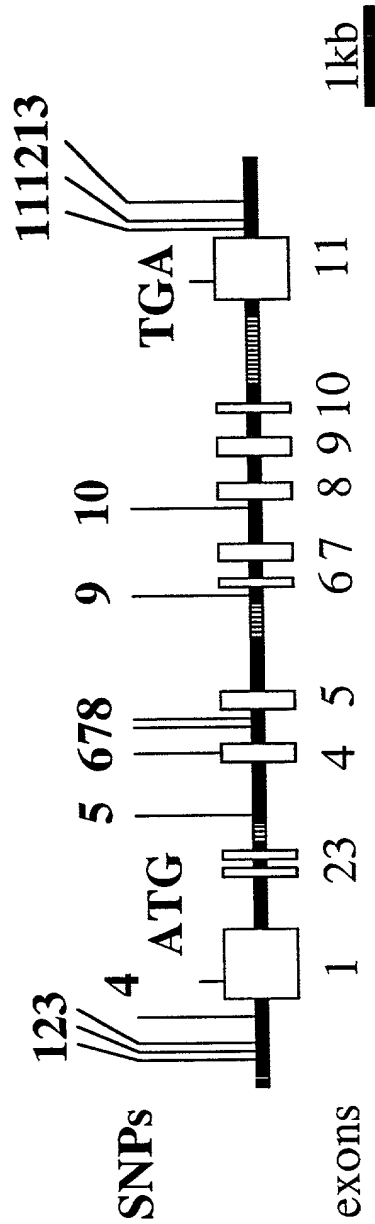


Fig. 180 *Transporter associated with antigen processing 2 (TAP2)*  
 ACCESSION X66401.1

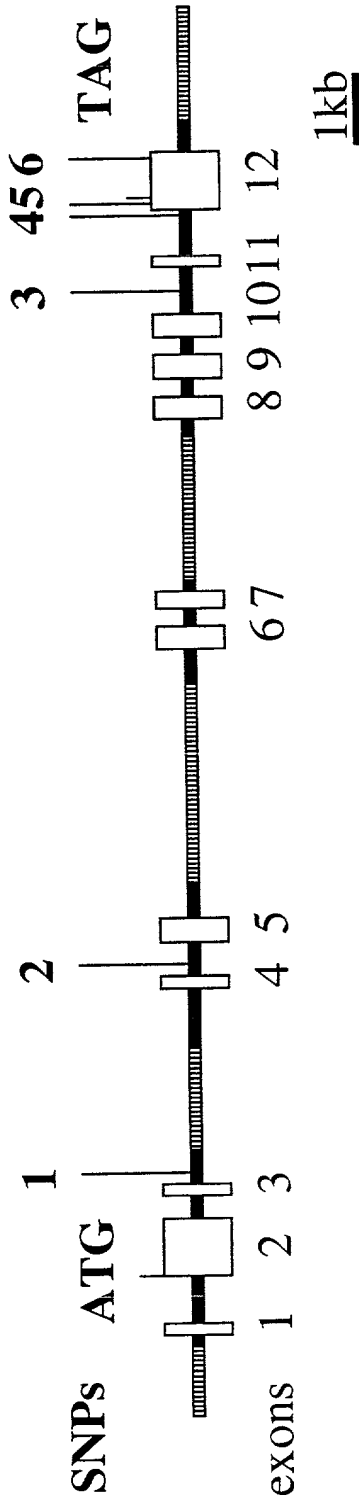




Fig. 181

*Solute carrier family 22, member 4 (SLC22A4)*  
*Organic cation transporter, member 4 (OCTN1)*

ACCESSION AC008599.6

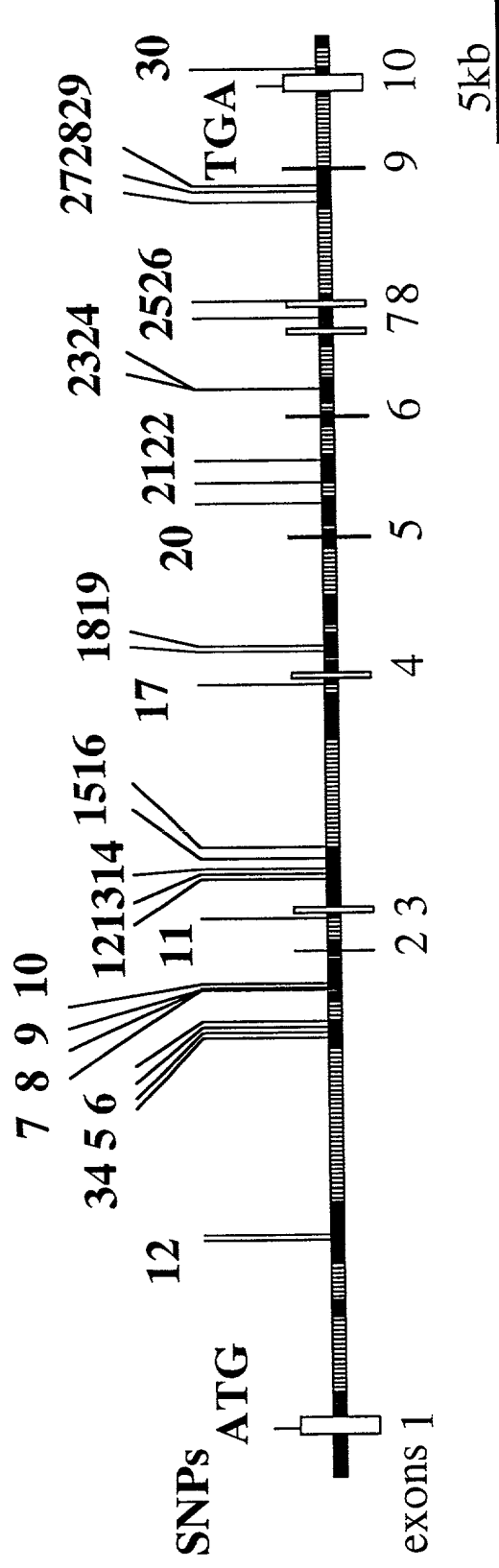


Fig. 182

*Solute carrier family 22, member 5 (SLC22A5)*  
*Organic cation transporter, member 5 (OCTN2)*

ACCESSION AC023861.3

ATG

123 45

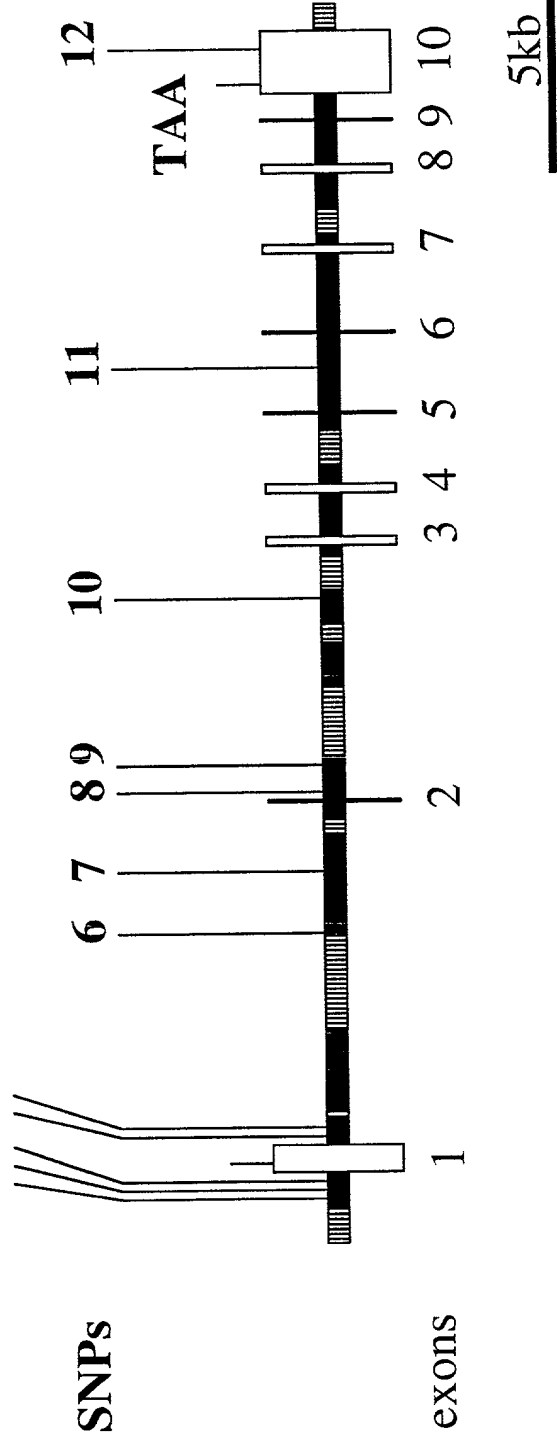


Fig. 183 Solute carrier family 22 (organic cation transporter), member 1  
(SLC22A1, OCT1) ACCESSION AL35625.5

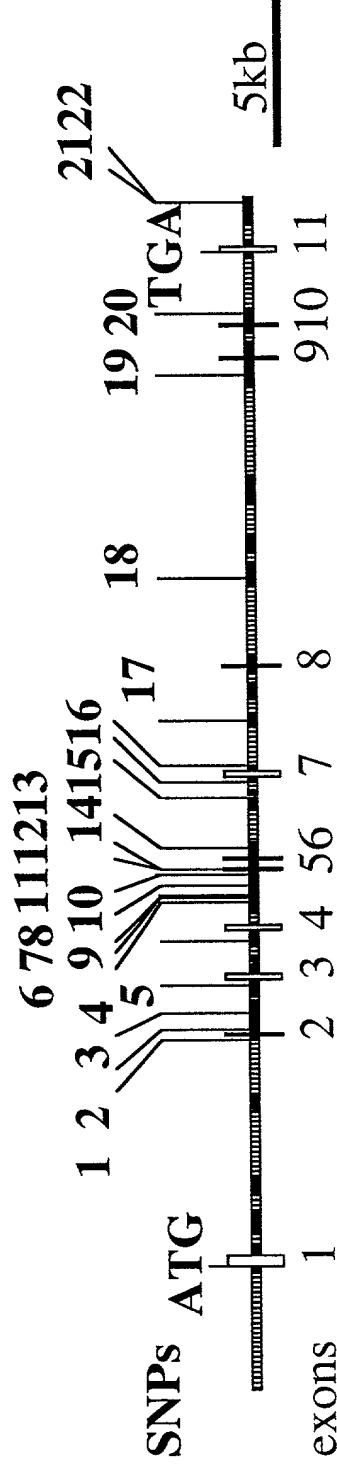


Fig. 184 Solute carrier family 22 (organic cation transporter), member 2  
(SLC22A2, OCT2) ACCESSION AL162582.18

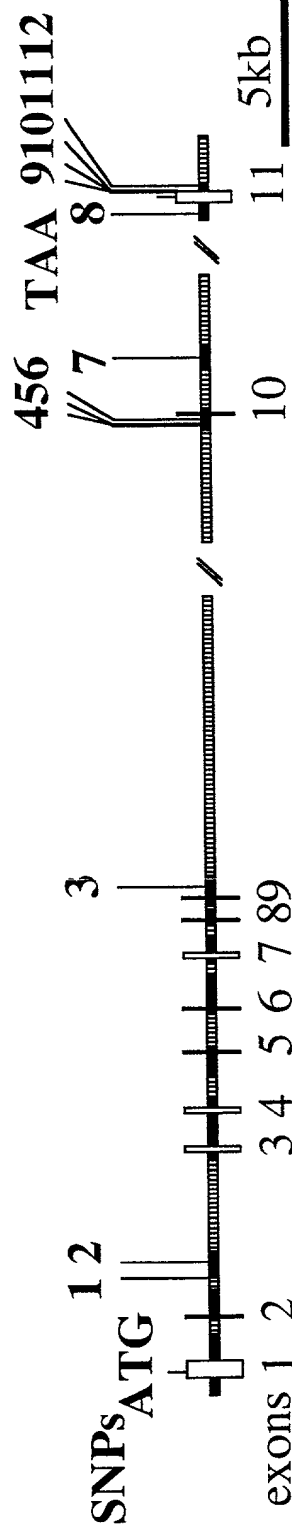


Fig. 185

*Solute carrier family 10, member 2 (SLC10A1)<sup>2</sup>*  
*Na/taurocholate cotransporting polypeptide (NTCP)*

ACCESSION AL157789.6

TAG

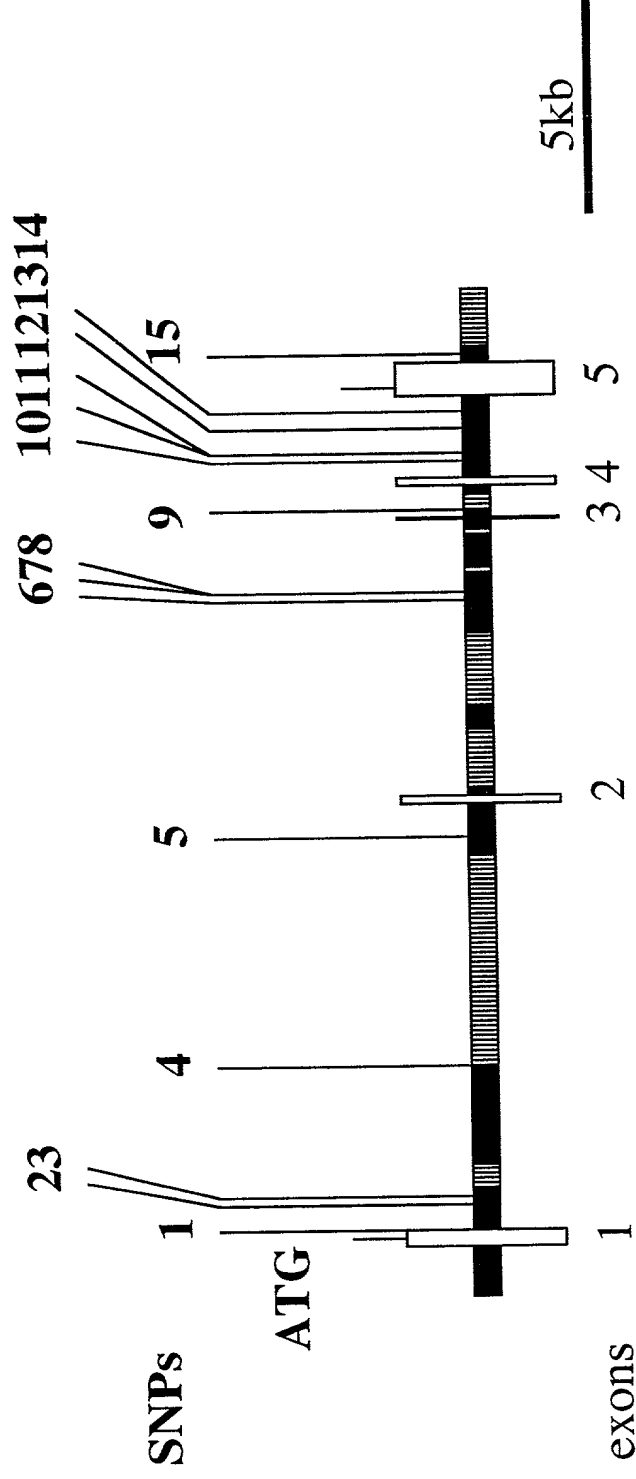


Fig. 186

*Solute carrier family 15, member 1 (SLC15A1)*  
*Oligopeptide transporter, member 1 (PEPT1)*

ACCESSION AL353574.8 AL391670.6

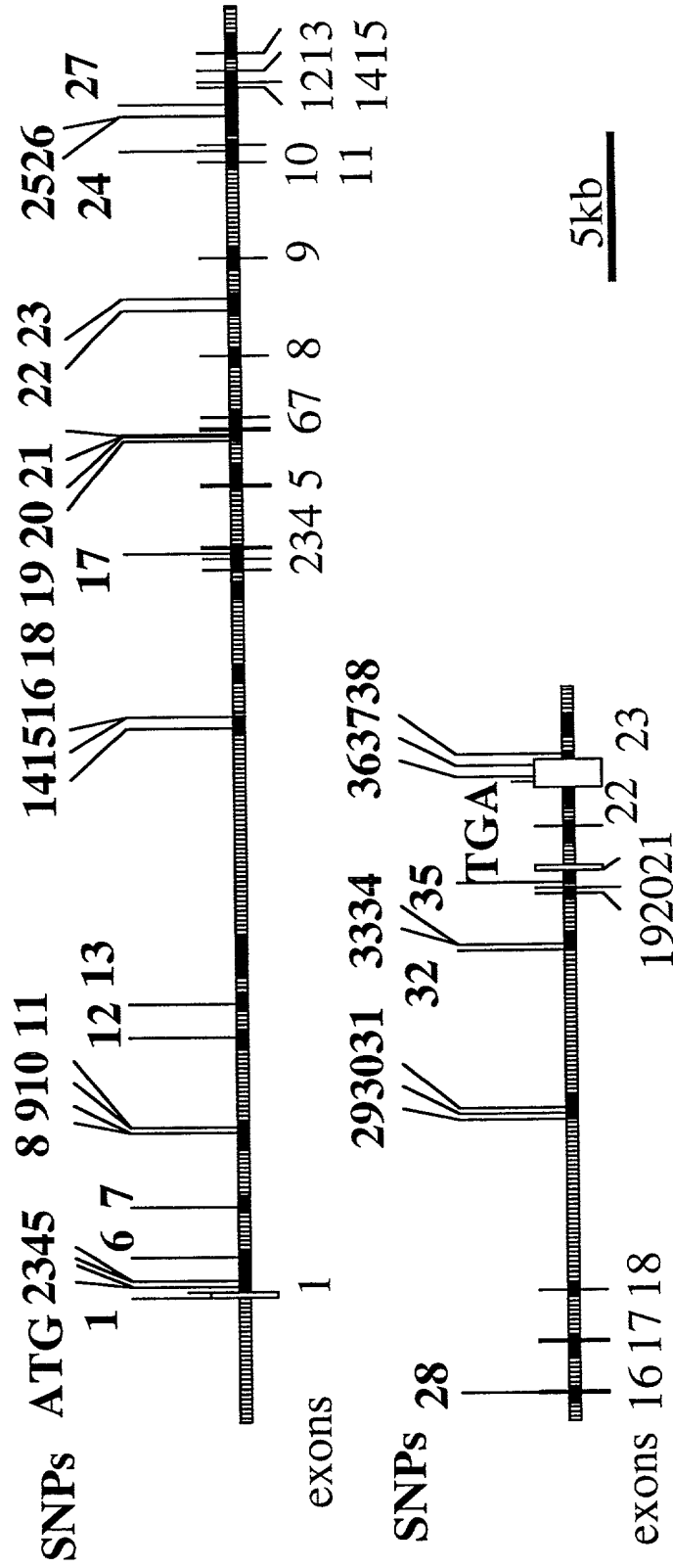


Fig. 187

*Epoxide hydrolase 1, microsomal (EPHX1)*

ACCESSION AC058782.8

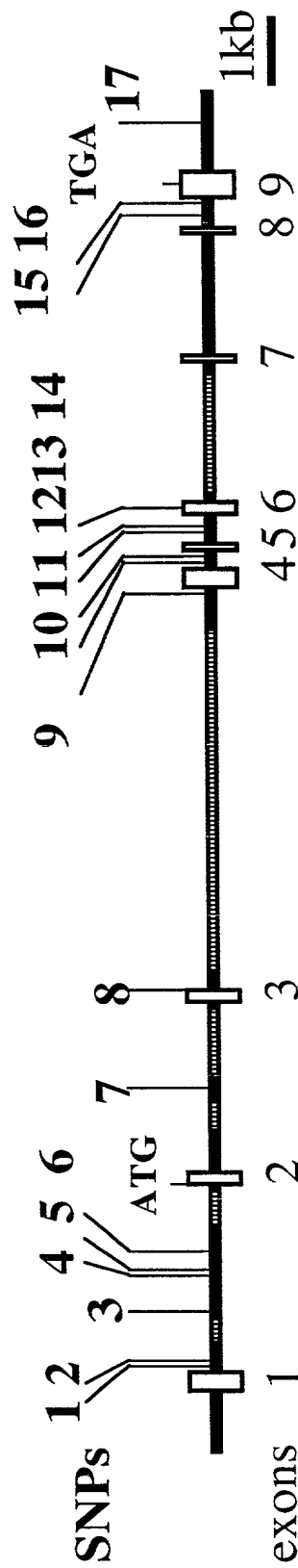


Fig. 188

*Epoxide hydrolase, cytoplasmic (EPHX2)*

ACCESSION AC010856.3

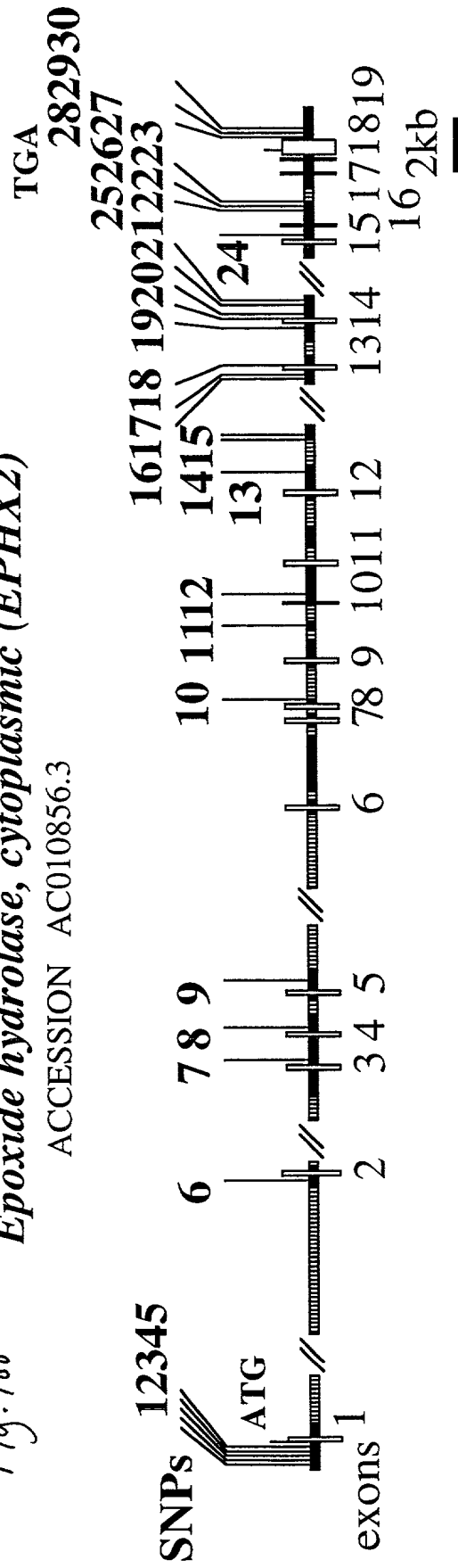


Fig. 189

# *Catechol-O-methyltransferase (COMT)*

ACCESSION AC000080.2

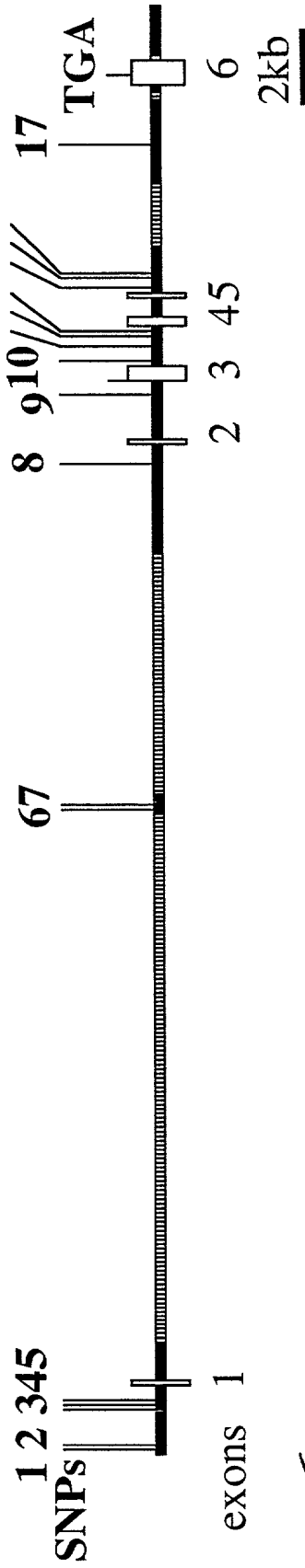


Fig. 190

# *Guanidinoacetate N-methyltransferase (GAMT)*

ACCESSION NT\_000879.1

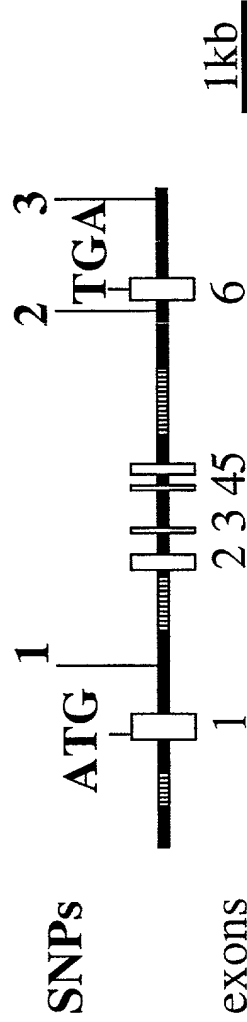
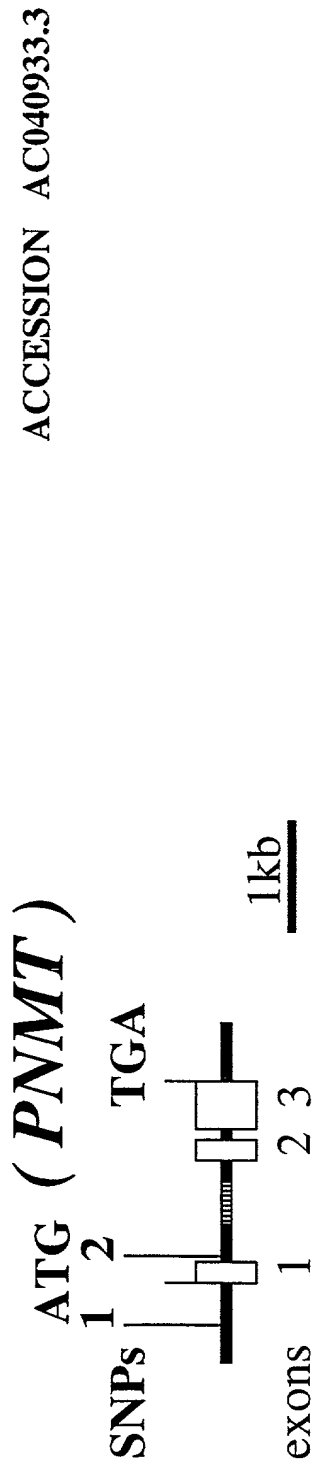


Fig. 191 *Phenylethanolamine N-methyltransferase*



ACCESSION AC040933.3

Fig. 192 *Histamine N-methyltransferase (HNMT)*

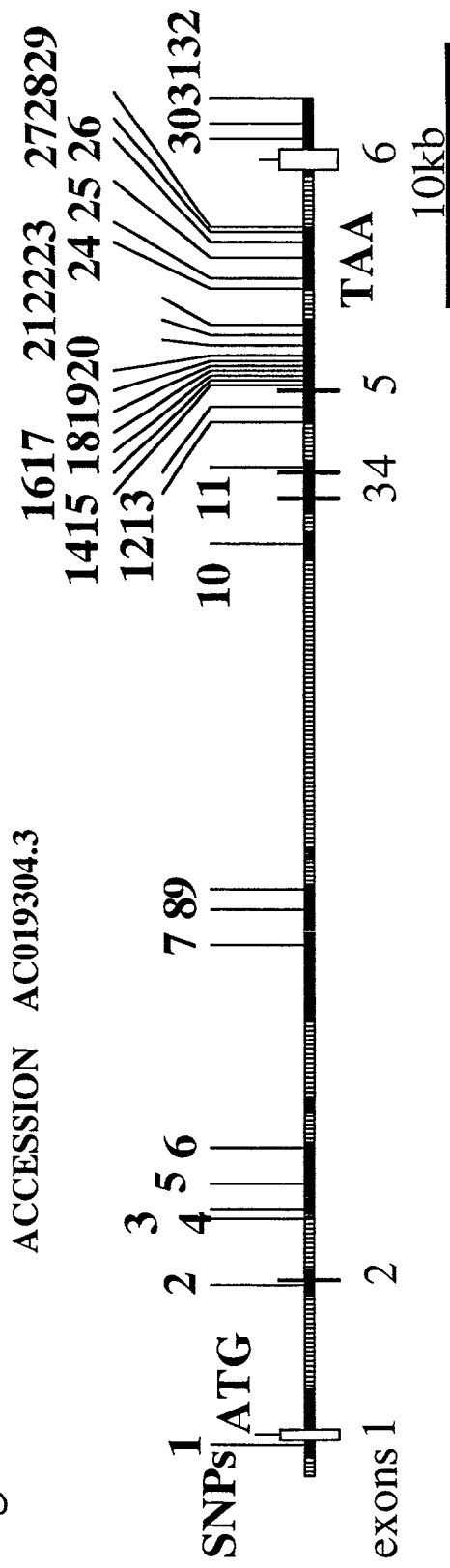




Fig. 193 Nicotinamide N-methyltransferase (NNMT)

ACCESSION AC019290.3

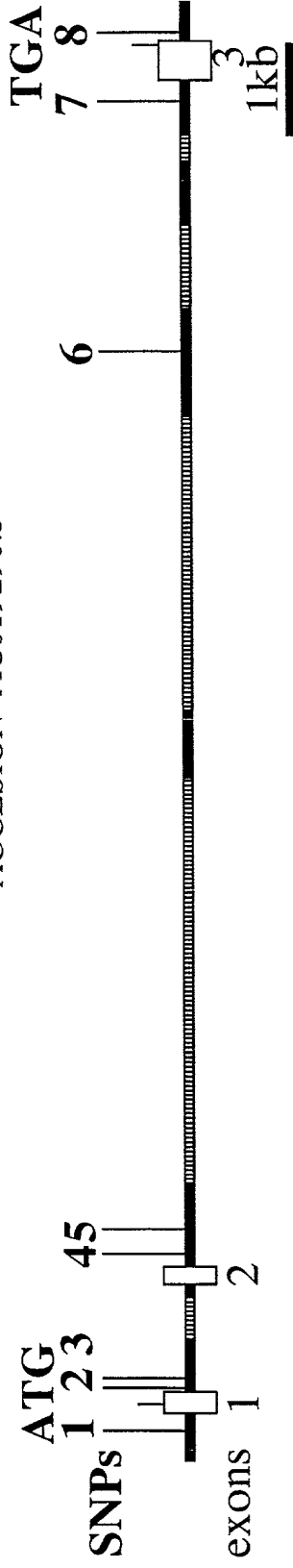


Fig. 194 Phosphatidylethanolamine N-methyltransferase (PEMT)

ACCESSION AC020558.3

TGA

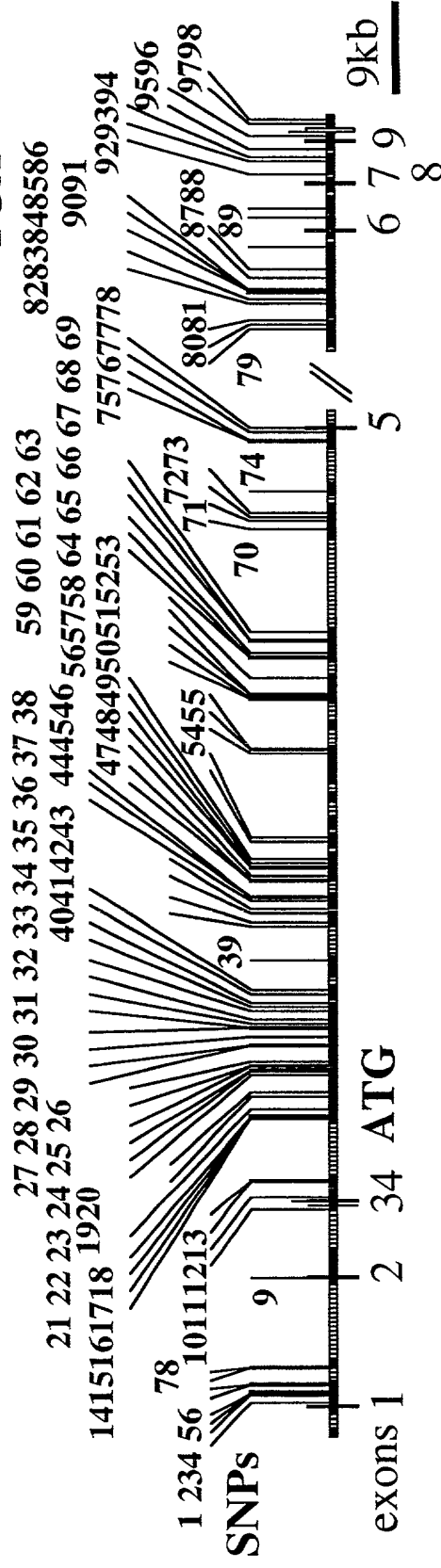
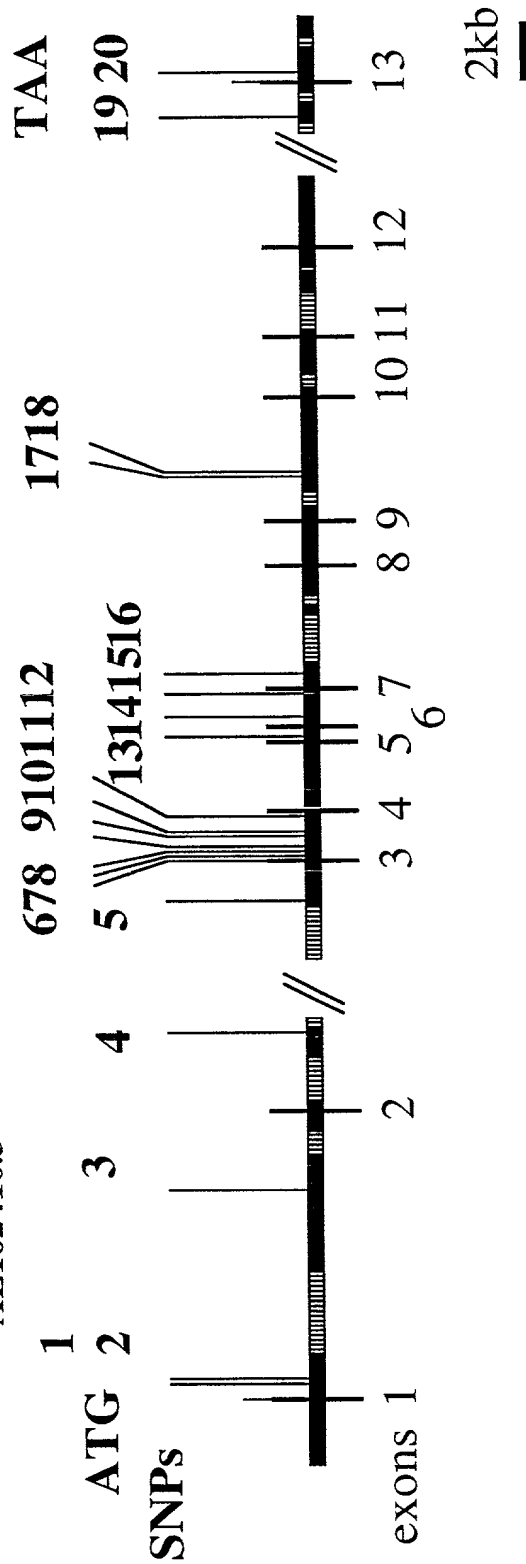


Fig. 195

*Aldehyde dehydrogenase 1 family,  
member A1 (ALDH1A1)*

ACCESSION AC009284.2  
AL162416.3



*Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2)*

ACCESSION AC025431.7

AC012653.8

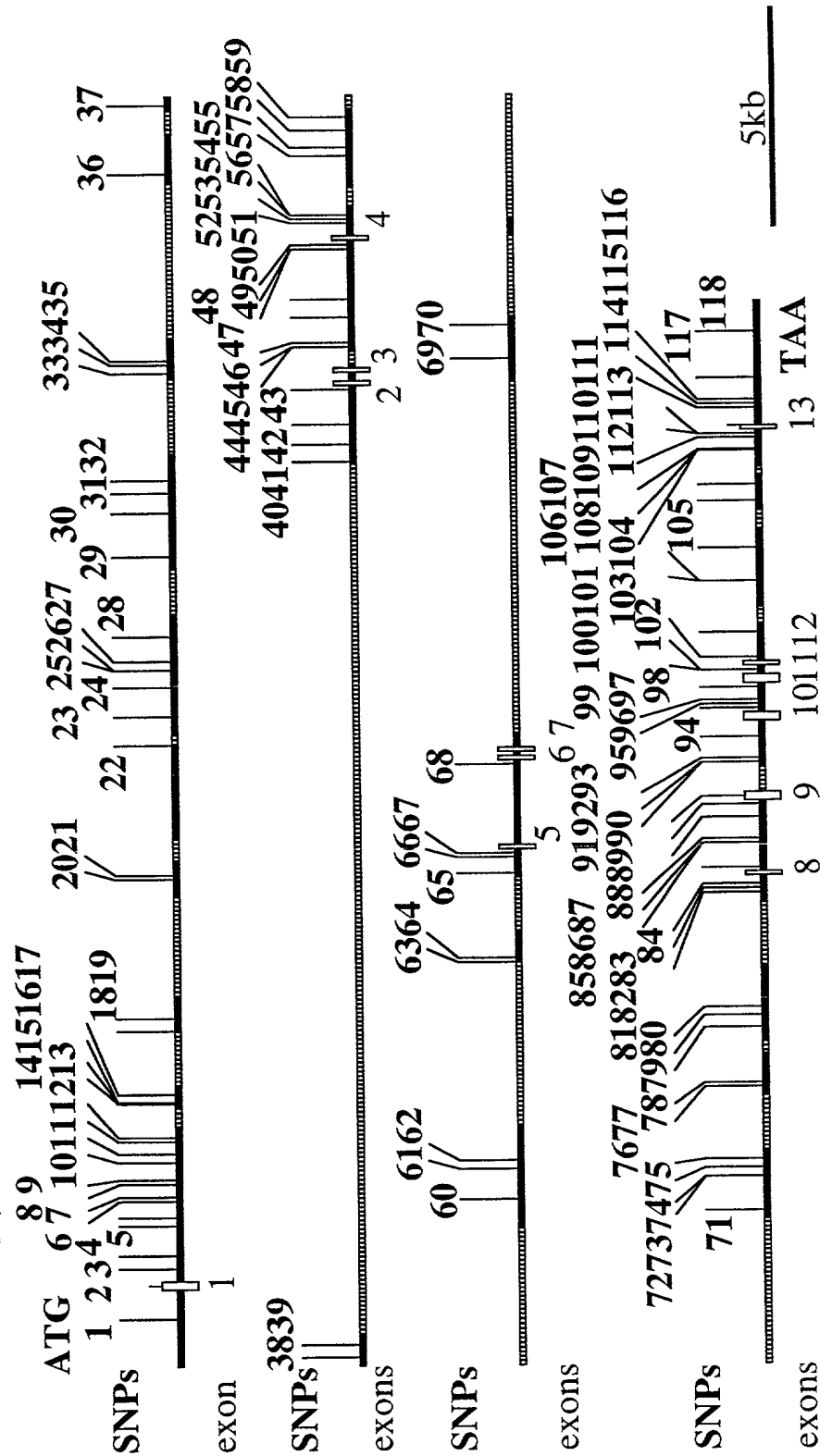


Fig. 197 *Aldehyde dehydrogenase 1 family, member A3 (ALDH1A3)*

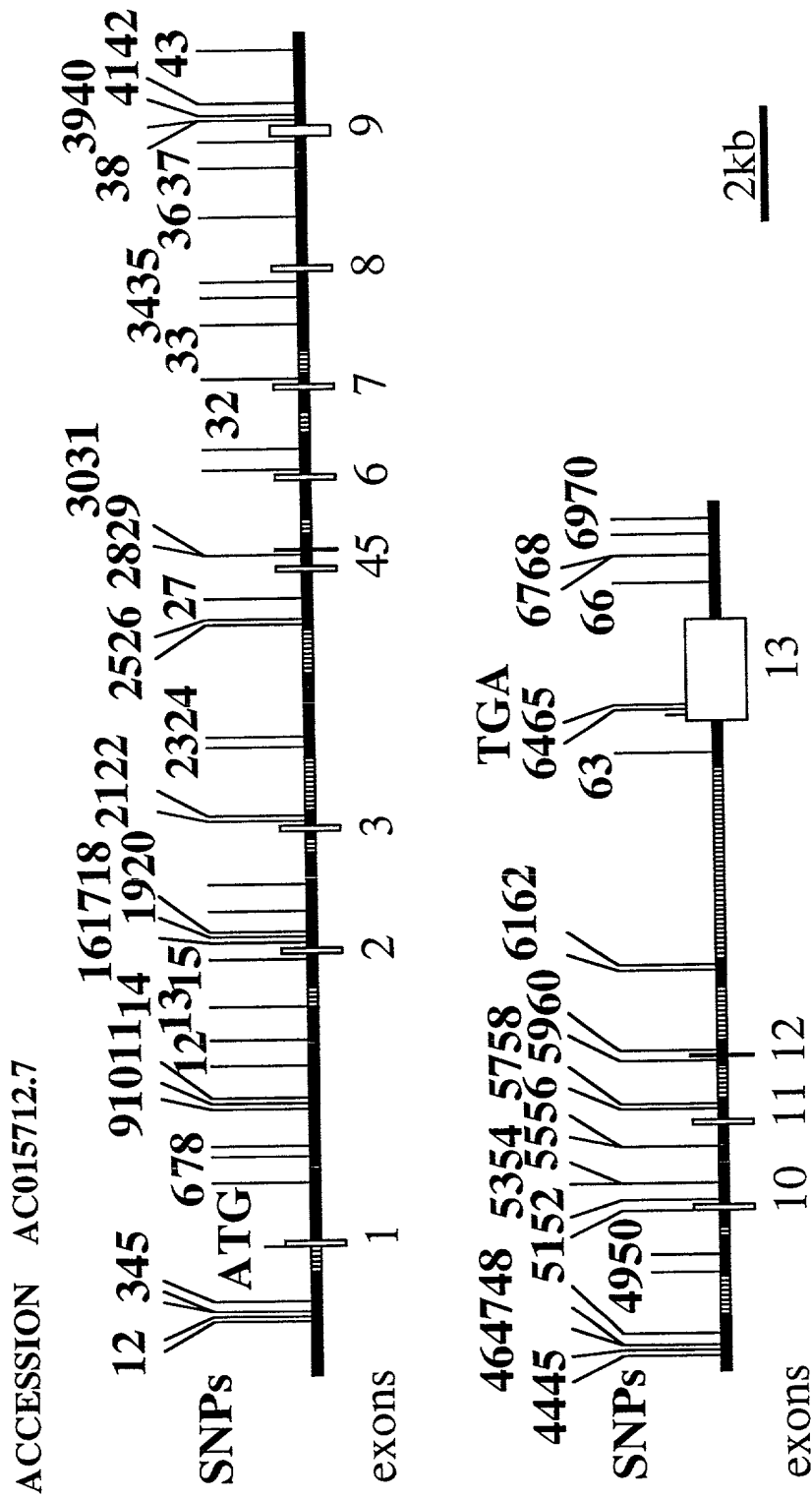


Fig. 198  
*Aldehyde dehydrogenase 1 family, member B1 (ALDH1B1)*

ACCESSION AL135785.9

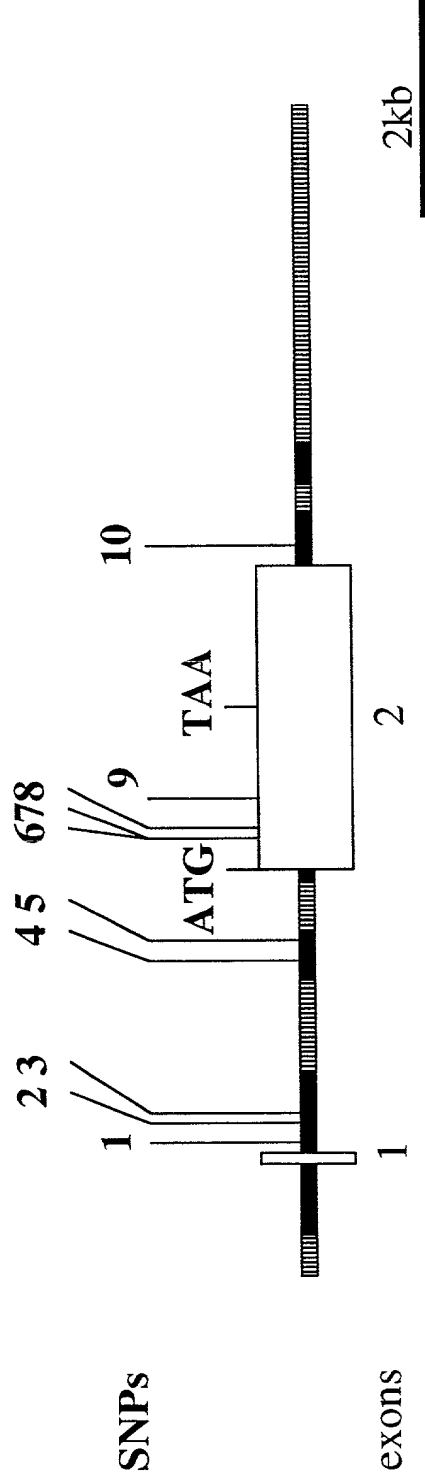


Fig. 199A *Formyltetrahydrofolate dehydrogenase (FTHFD)*  
*Aldehyde dehydrogenase 1 family, member L1 (ALDH1L1)*

ACCESSION AC079848.6

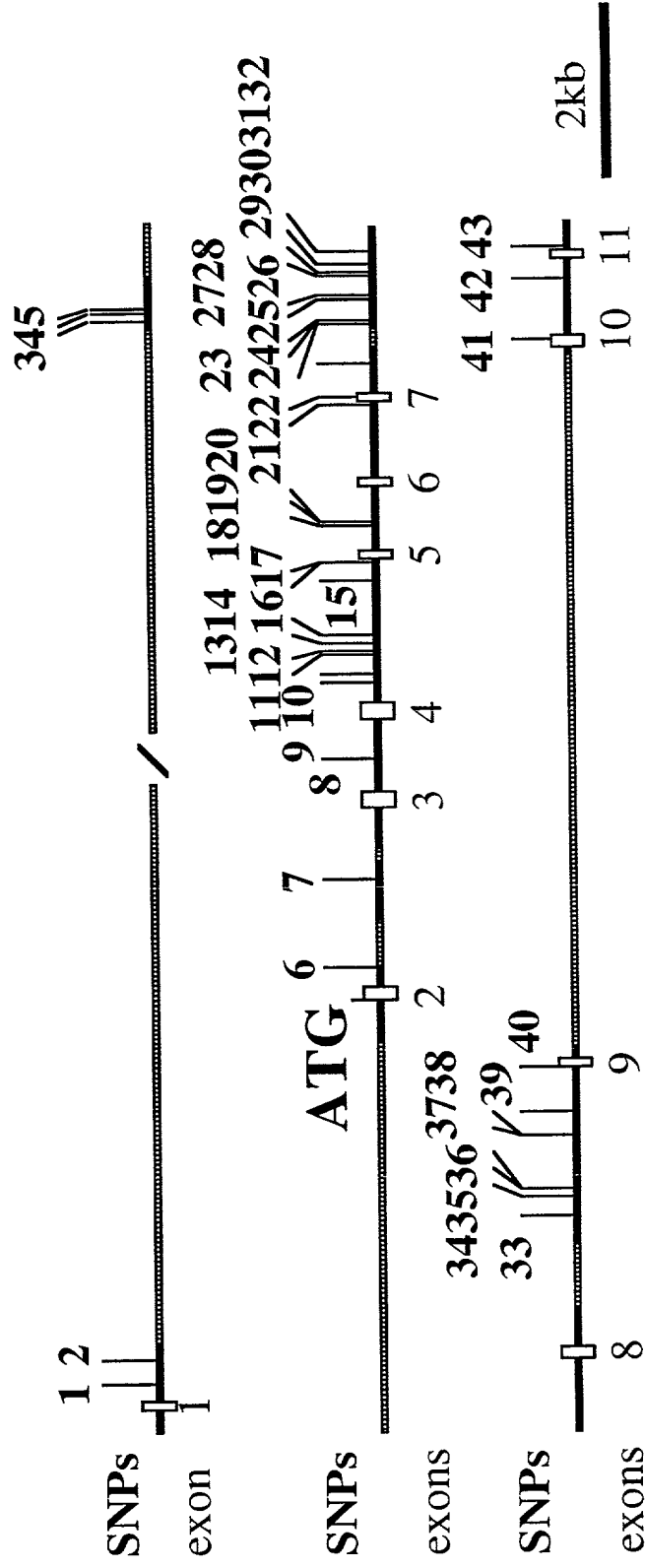


Fig. 199B

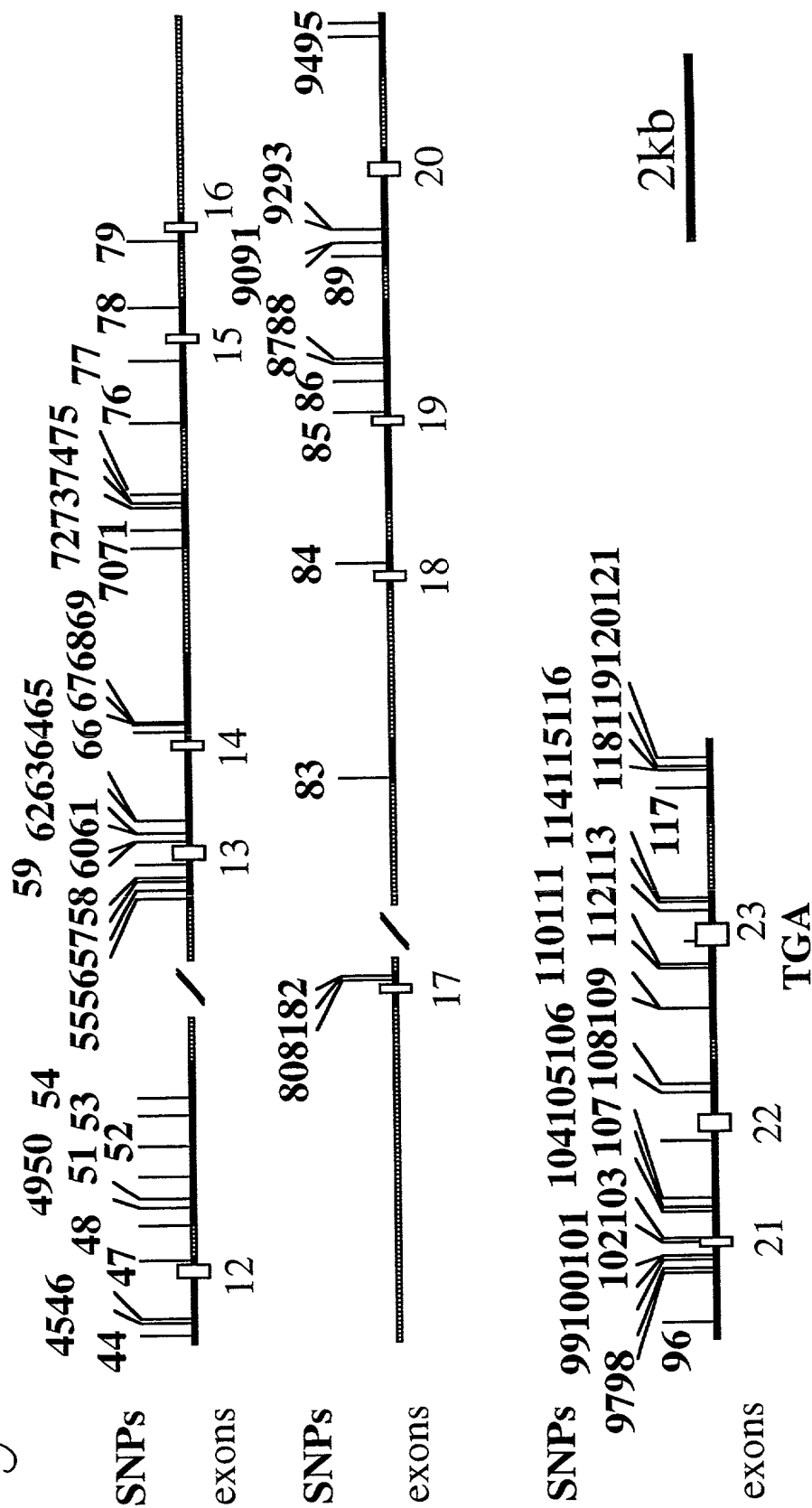


Fig. 200 Aldehyde dehydrogenase 2 (ALDH2)

ACCESSION AC002996.1  
AC003029.2

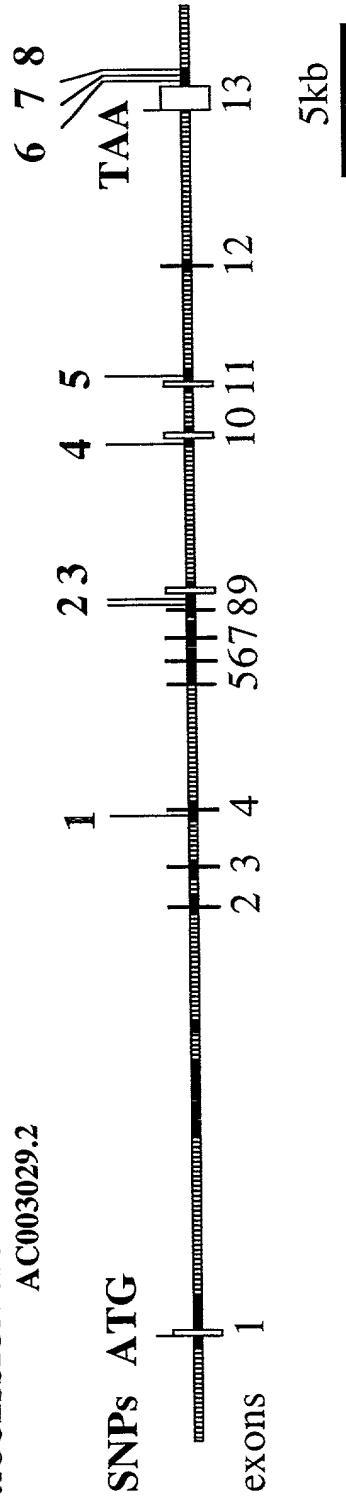


Fig. 201 Aldehyde dehydrogenase 3 family, member A1 (ALDH3A1)

ACCESSION AC005722.1

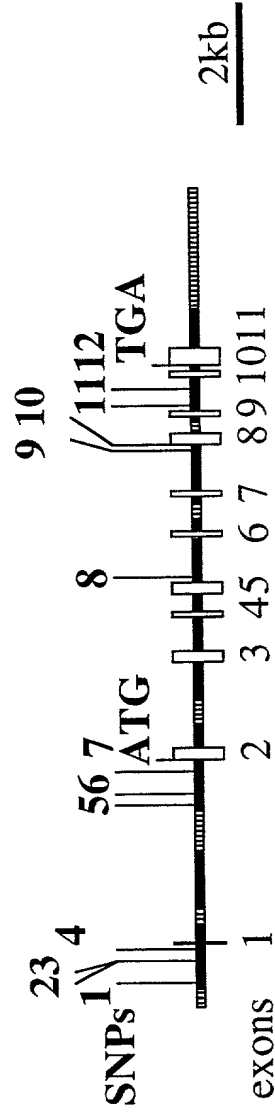




Fig. 202 Aldehyde dehydrogenase 3 family, member A2  
(ALDH3A2) ACCESSION AC005722.1

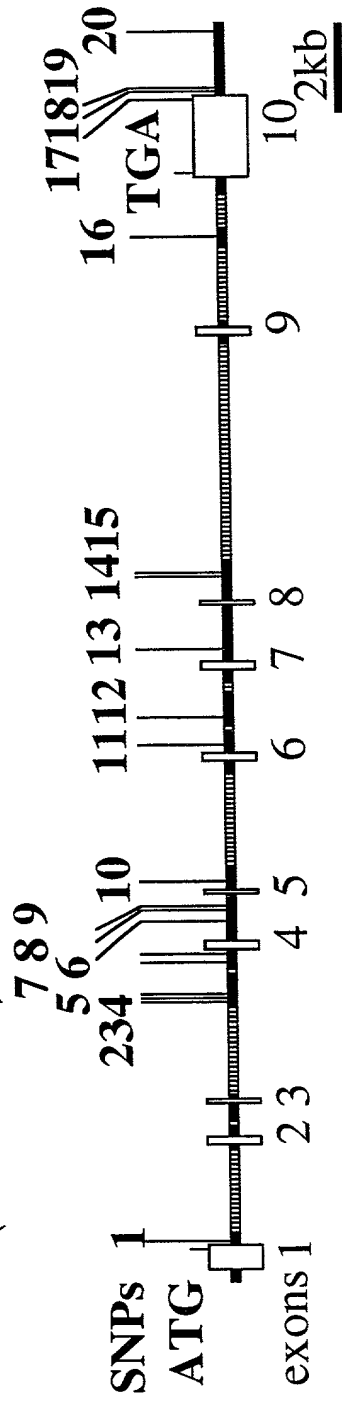


Fig. 203 Aldehyde dehydrogenase 3 family, member B1 (ALDH3B1)  
ACCESSION AC004923.2

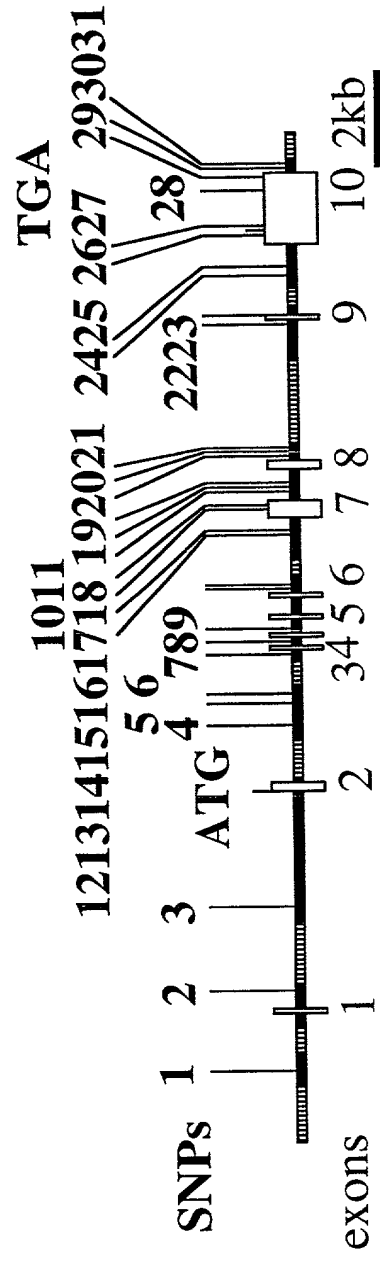


Fig. 204 Aldehyde dehydrogenase 3 family, member B2 (ALDH3B2)

ACCESSION AC021987.3

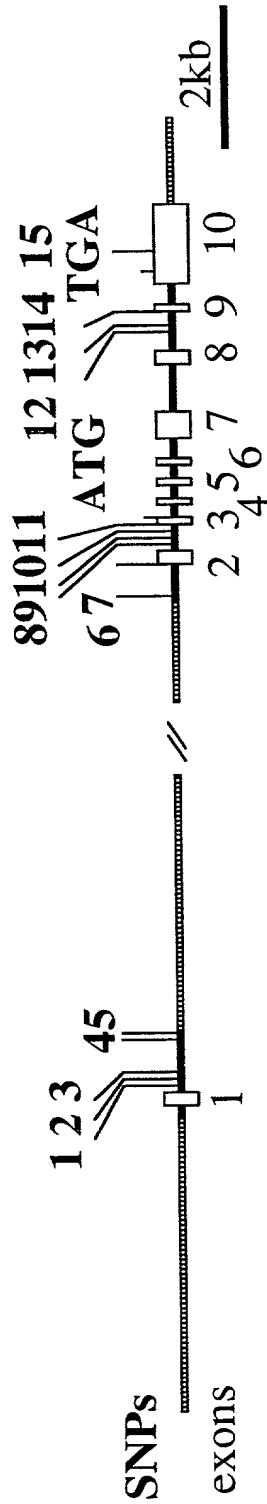


Fig. 205 Aldehyde dehydrogenase 5 family, member A1 (ALDH5A1)

ACCESSION AL031230.1

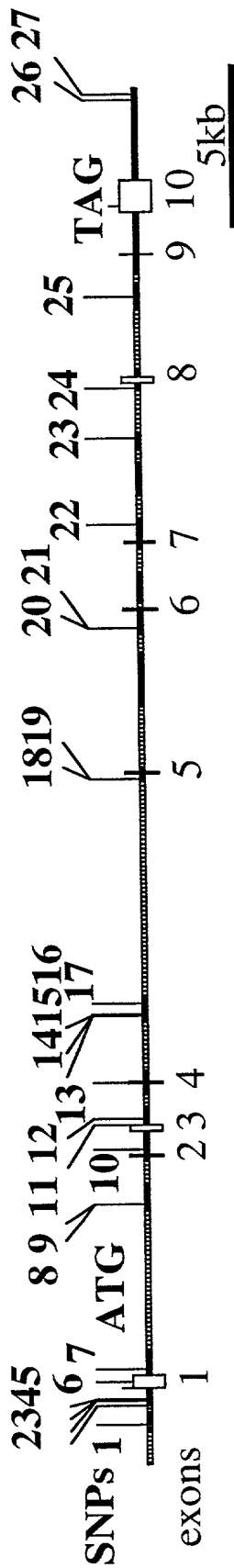


Fig. 206 Aldehyde dehydrogenase 6 family, member A1 (ALDH6A1)

ACCESSION AC005484.2

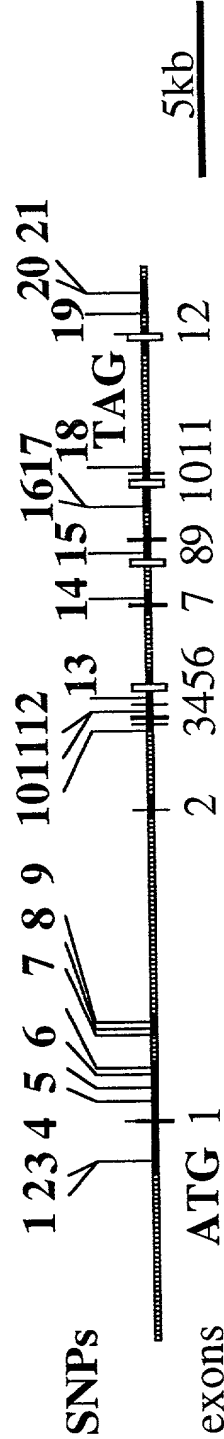


Fig. 207 *Aldehyde dehydrogenase 8 family, member A1 (ALDH8A1)*      ACCESSION AL445190.9  
AL021939.1

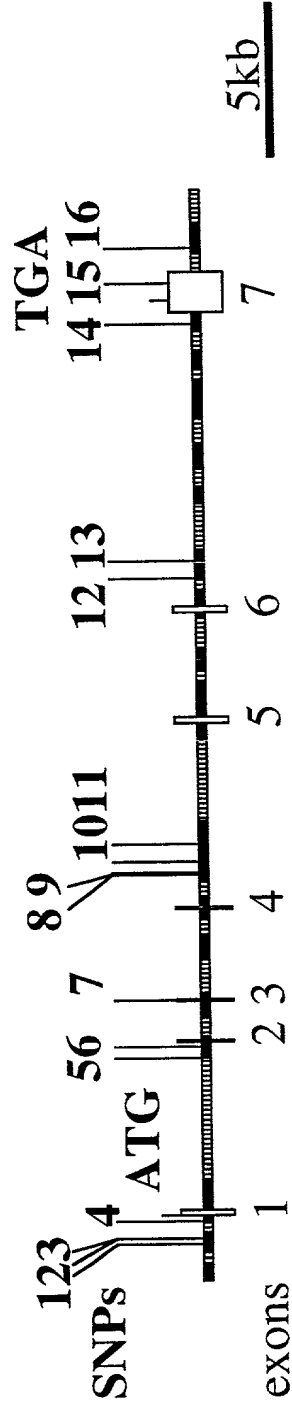


Fig. 208 *Aldehyde dehydrogenase 9 family, member A1 (ALDH9A1)*      ACCESSION AL451074.4

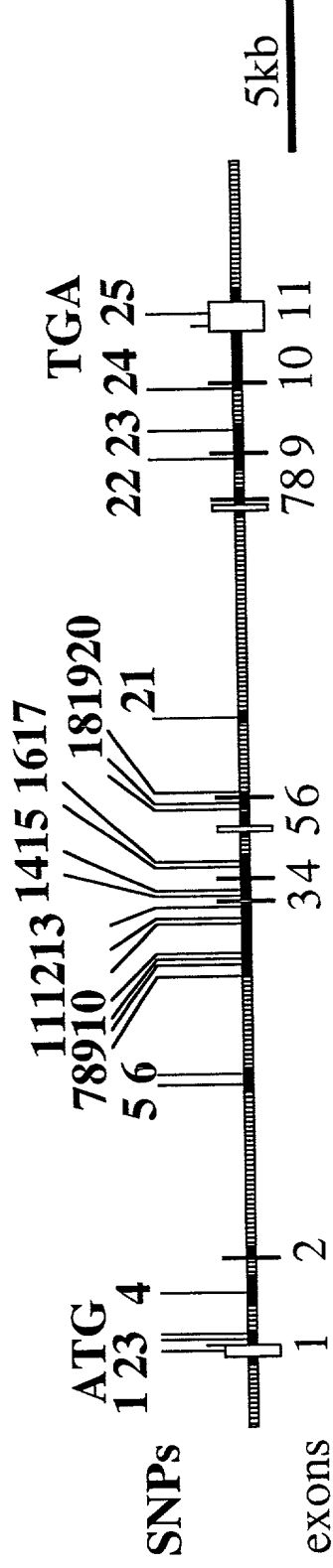


Fig. 209 Alcohol dehydrogenase 1 (*ADH1*)

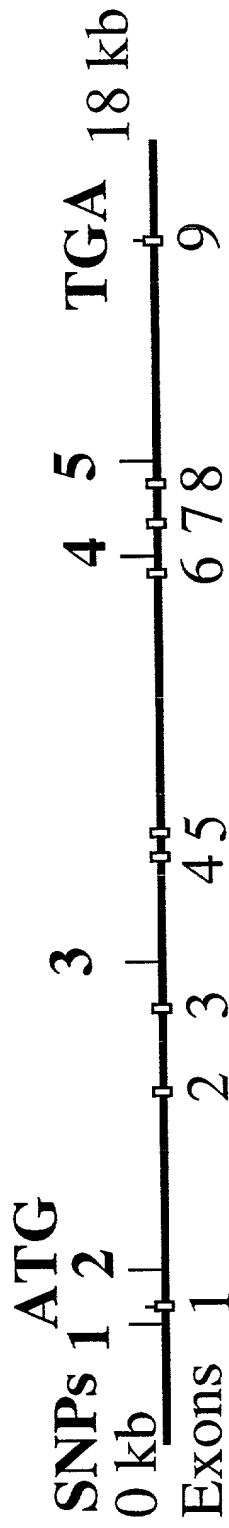


Fig. 210 Alcohol dehydrogenase 2 (*ADH2*)

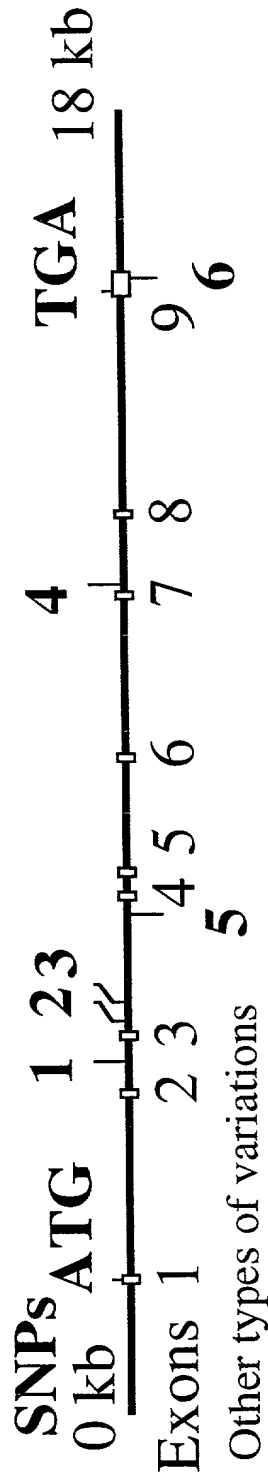


Fig. 211 Alcohol dehydrogenase 3 (*ADH3*)

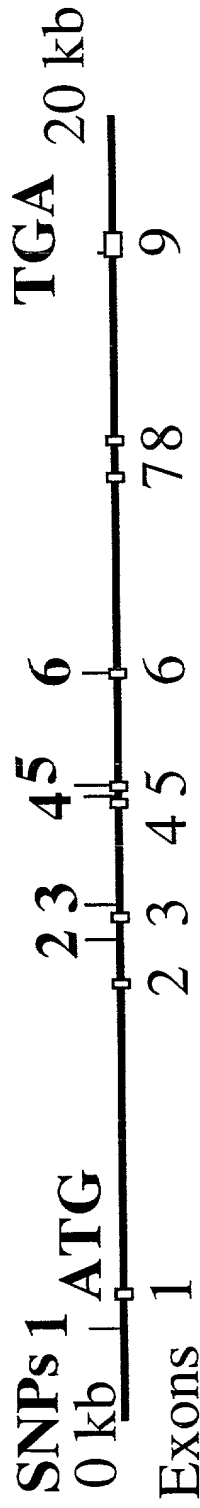
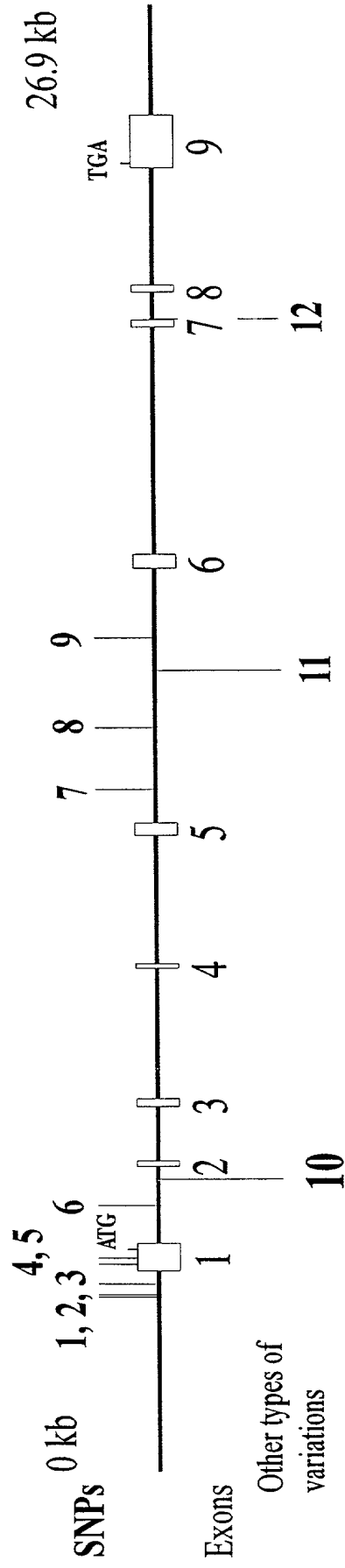


Fig. 212

Alcohol dehydrogenase 4 (*ADH4*)



## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AGCCTCAGTT TCTCTTTGGT GTTCCCGCCC ACAGTTCCCG CTGTACTGGT TCAGCGTGCC  
Observed : A/G  
3' Assay : GCCATCCTGA AGGCTGGAT GGATAGGGTG CTGTGCCAGG GCTTTGCCTT TGACATCCCA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 (Graphical View of this Entry)  
Chromosome : 6  
map :  
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
Position in Sequence : 171597 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_026300.1.20010416.9  
Amplified region size : 171031..172143 in NT\_026300 : 1113  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

Fig. 216 Short-chain alcohol dehydrogenase family gene  
(HEP27)

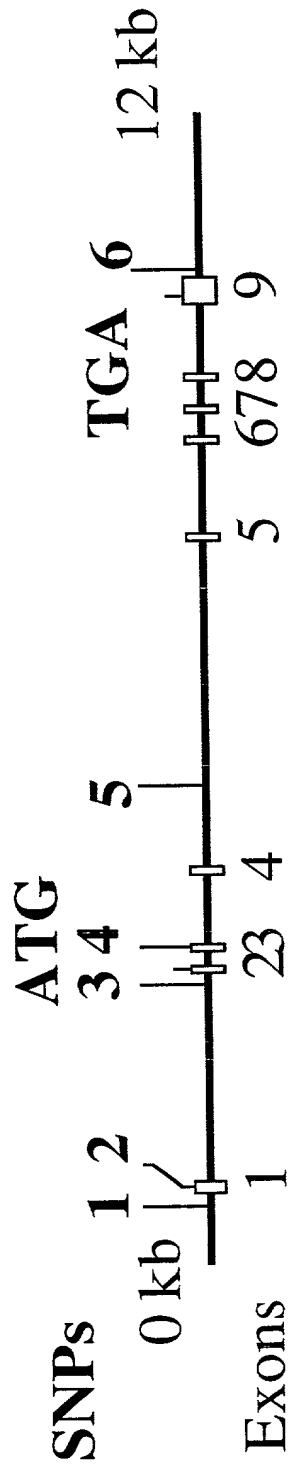


Fig. 2/17

**UDP glycosyltransferase 1 family, peptide A1  
(*UGT1A1*)**

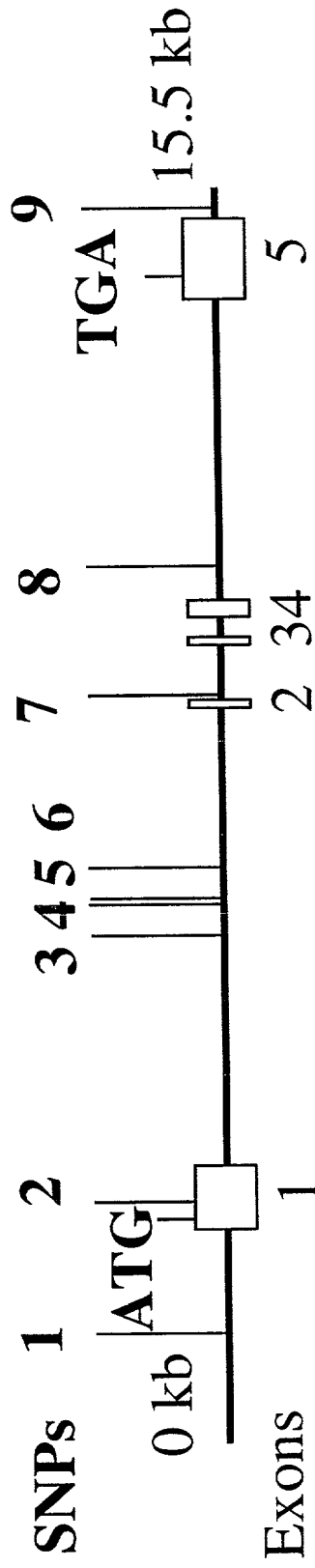




Fig. 218

UDP glycosyltransferase 2 family, polypeptide A1 (UGT2A1)

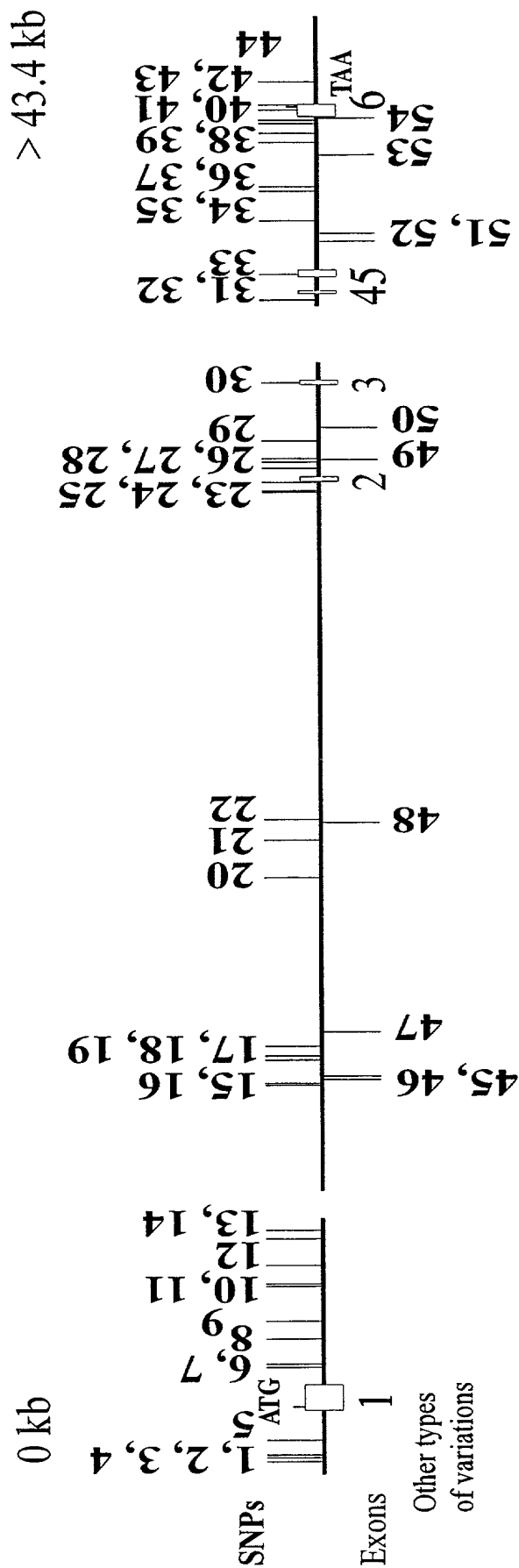


Fig. 219

UDP-glycosyltransferase 2 family, polypeptide B15(*UGT2B15*)

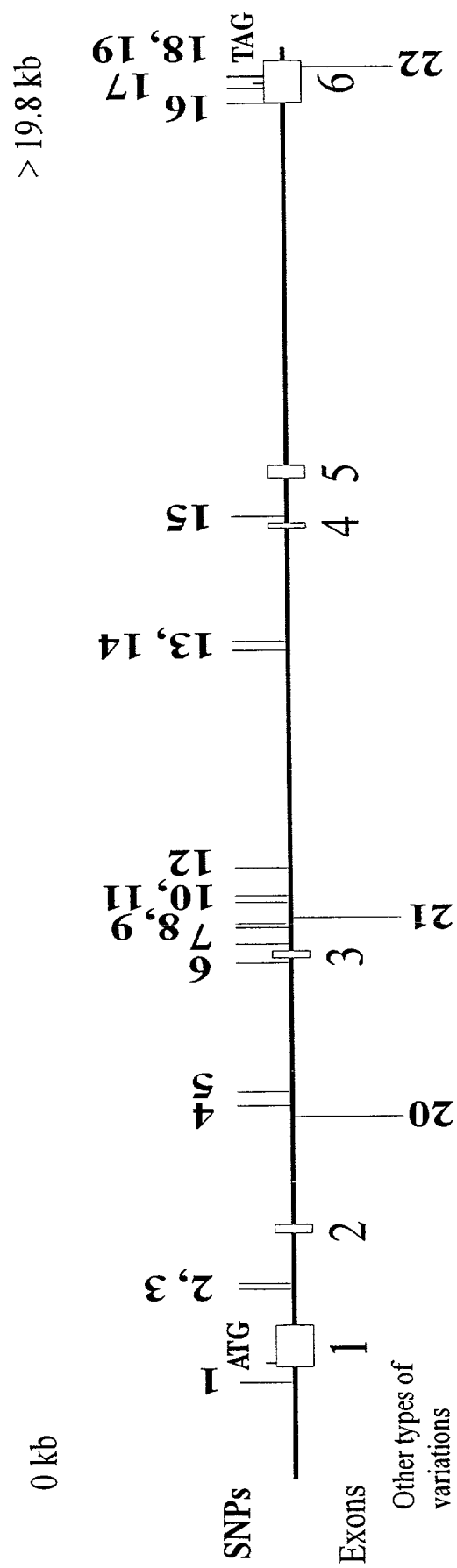


Fig. 220

# UDP glycosyltransferase 8 (*UGT8*)

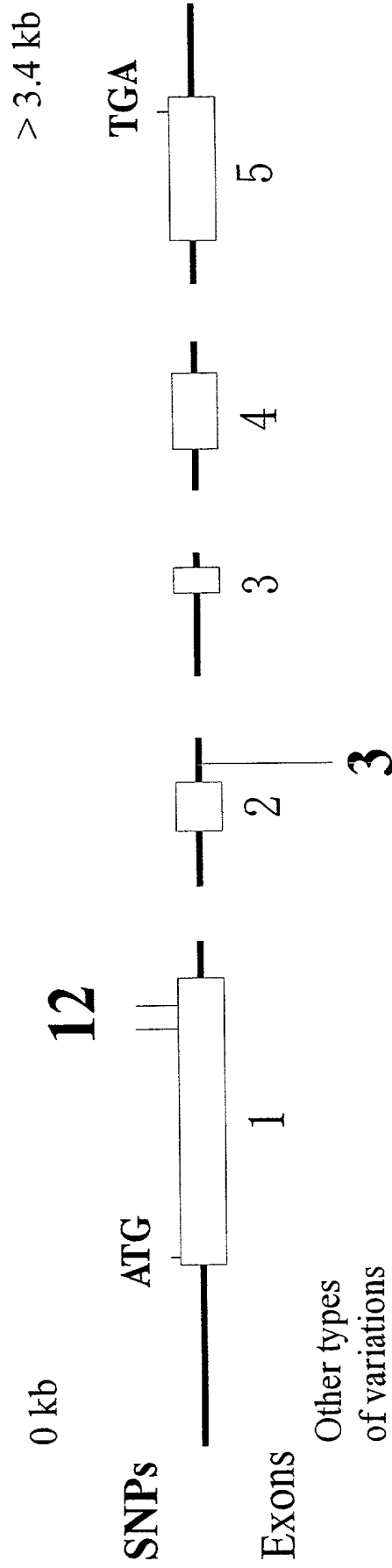


Fig. 221

# Glutathione S-transferase A1 (*GSTA1*)

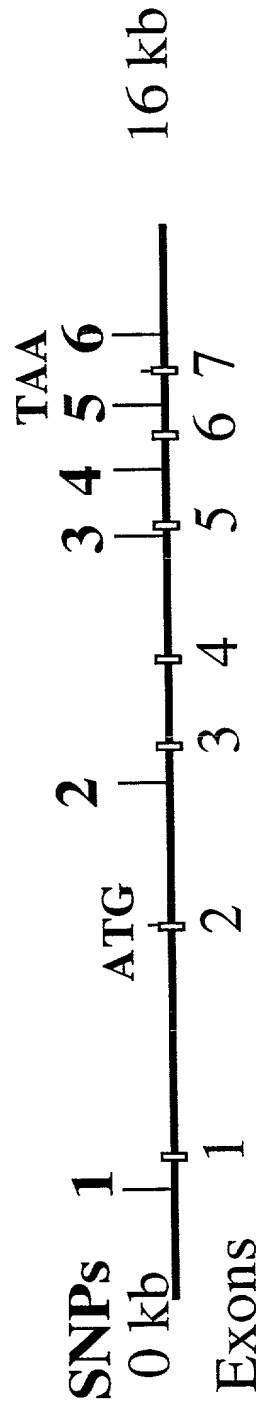


Fig. 222

# Glutathione S-transferase A4 (*GSTA4*)

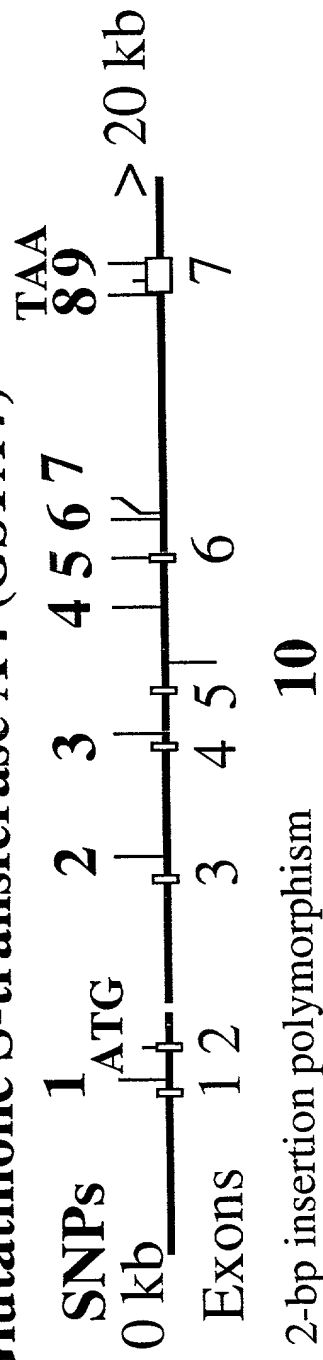


Fig. 223

Glutathione S-transferase M1 (*GSTM1*)

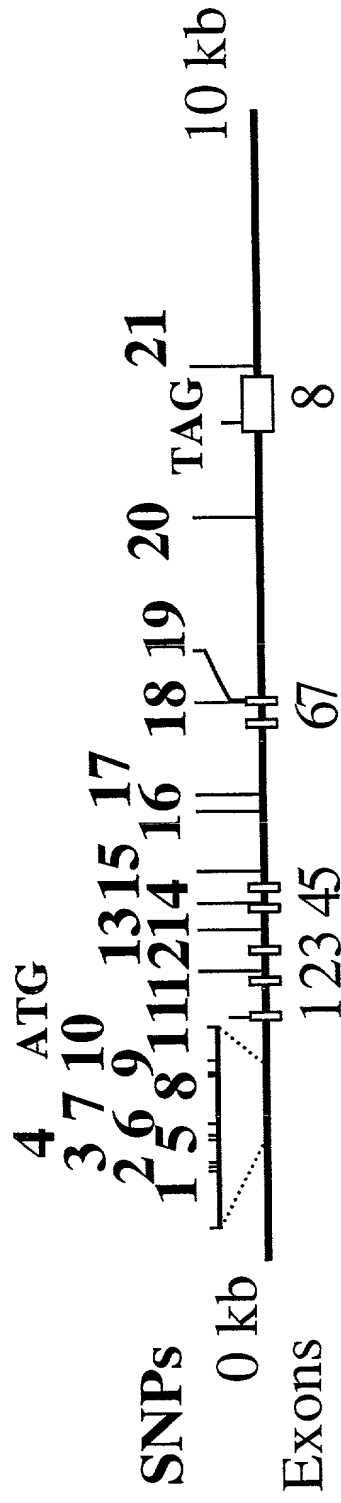


Fig. 224

Glutathione S-transferase M2 (*GSTM2*)

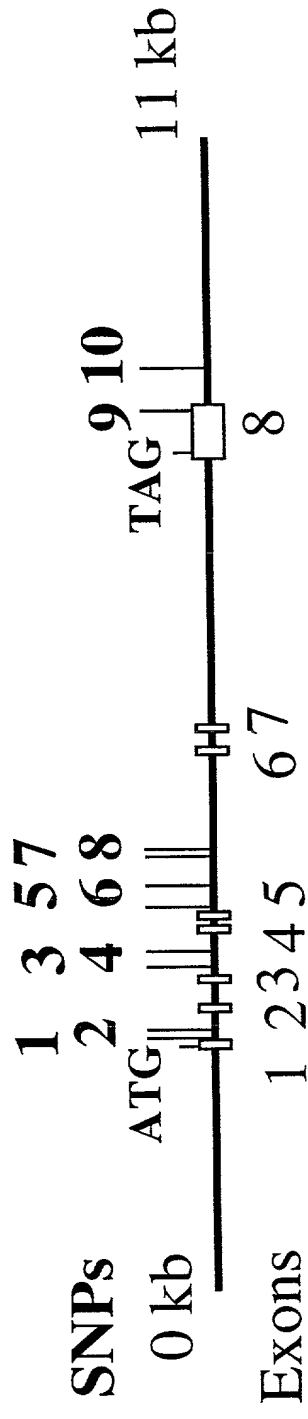


Fig. 225

Glutathione S-transferase zeta 1 (*GSTZ1*)

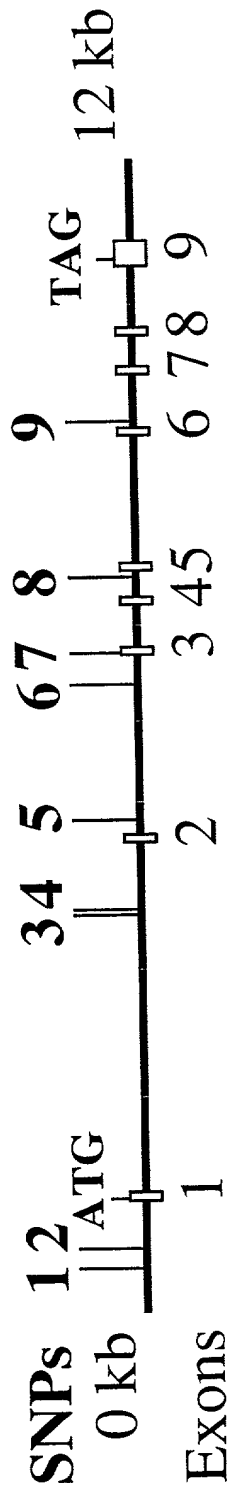


Fig. 226

Glutathione S-transferase pi (*GSTPi*)

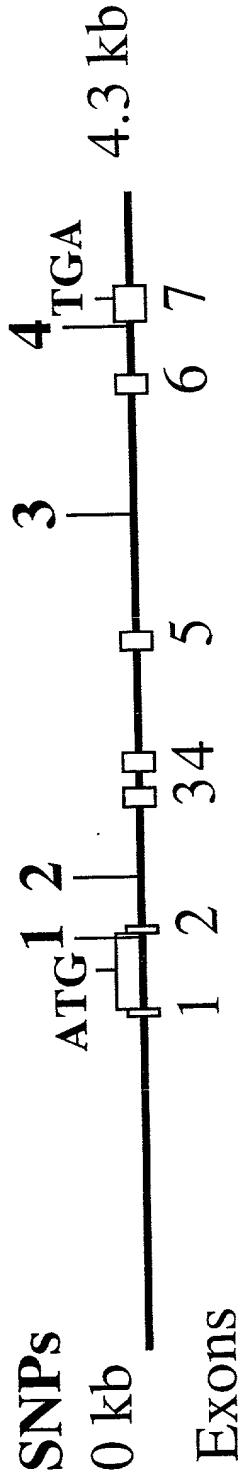


Fig. 227

# Glutathione S-transferase theta 1 (*GSTT1*)

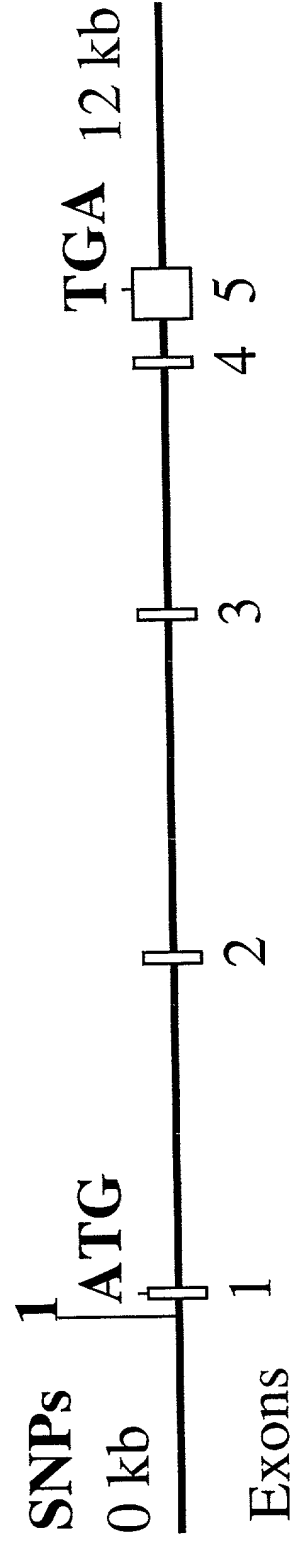


Fig. 228  
Microsomal glutathione S-transferase 1 (*MGST1*)

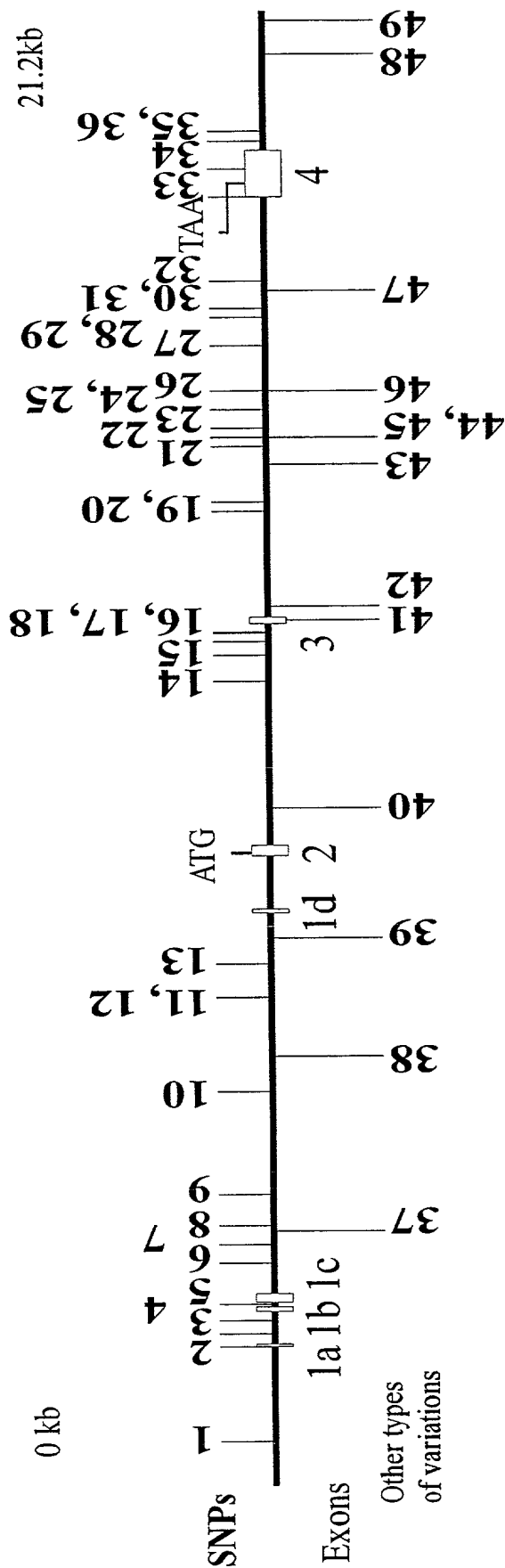




Fig. 229

Microsomal glutathione S-transferase 1-like 1 (*MGST1L1*)



Fig. 230

Microsomal glutathione S-transferase 2 (*MGST2*): AC019049.4

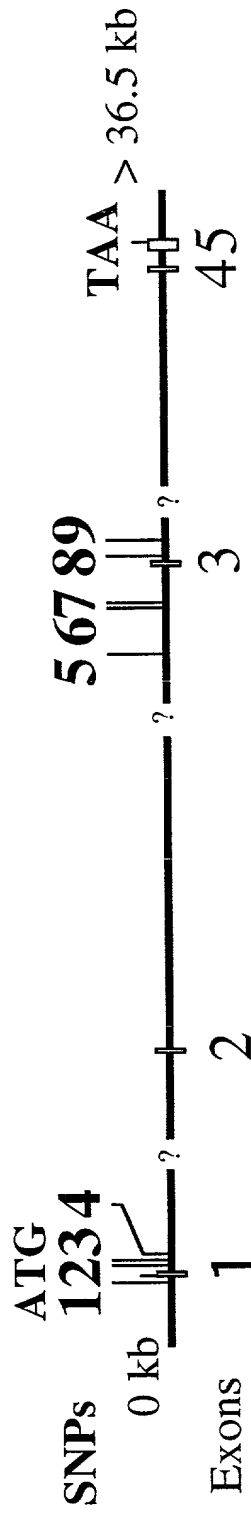


Fig. 231

# Microsomal glutathione S-transferase 3 (*MGST3*)

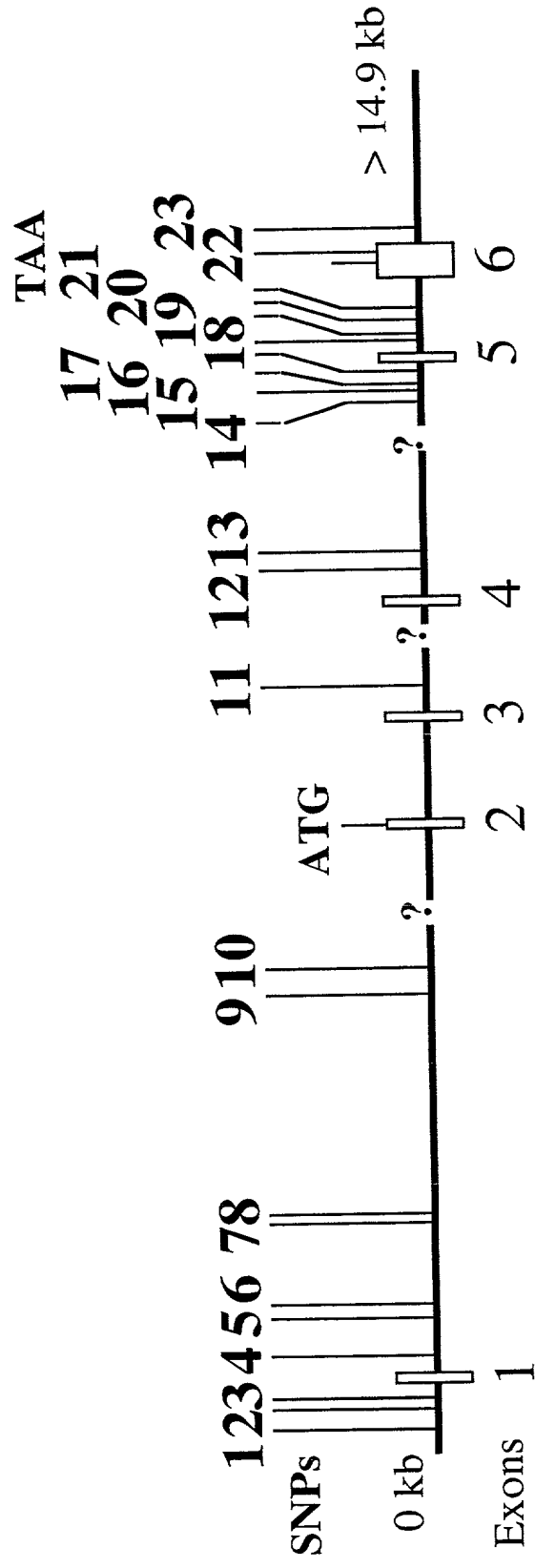


Fig. 232

# Sulfotransferase 1A1 (*SULT1A1/STP1*)

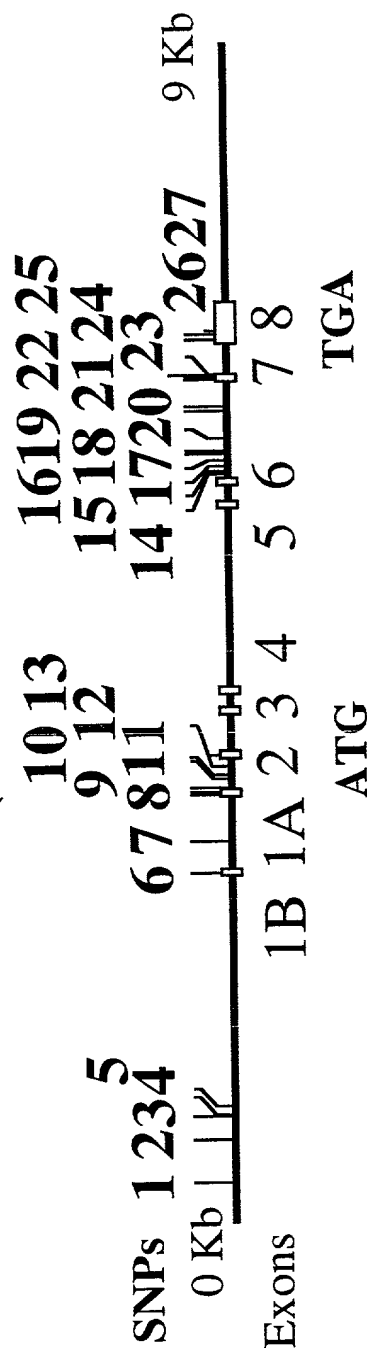


Fig. 233

# Sulfotransferase 1A2 (*SULT1A2/STP2*)

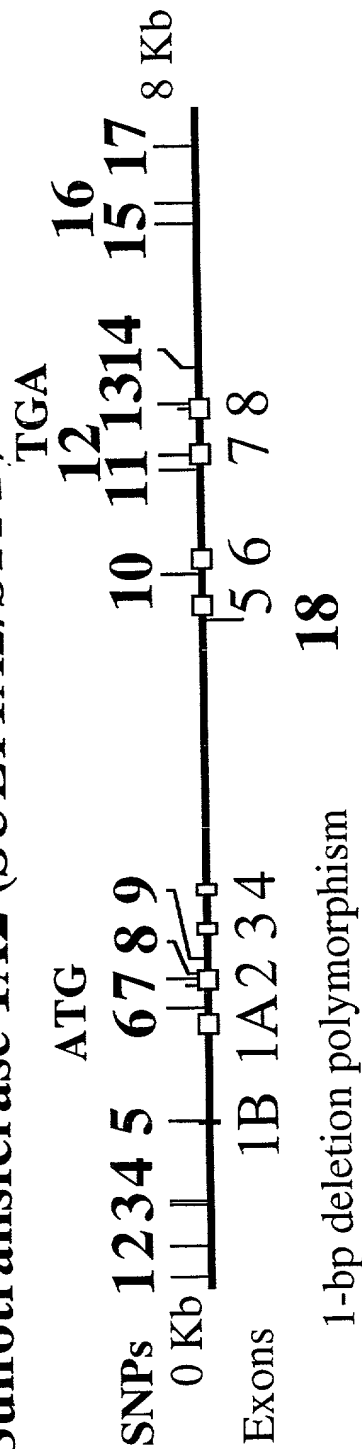


Fig. 234

Sulfotransferase 1A3 (*SULT1A3*/STM/ HAST)

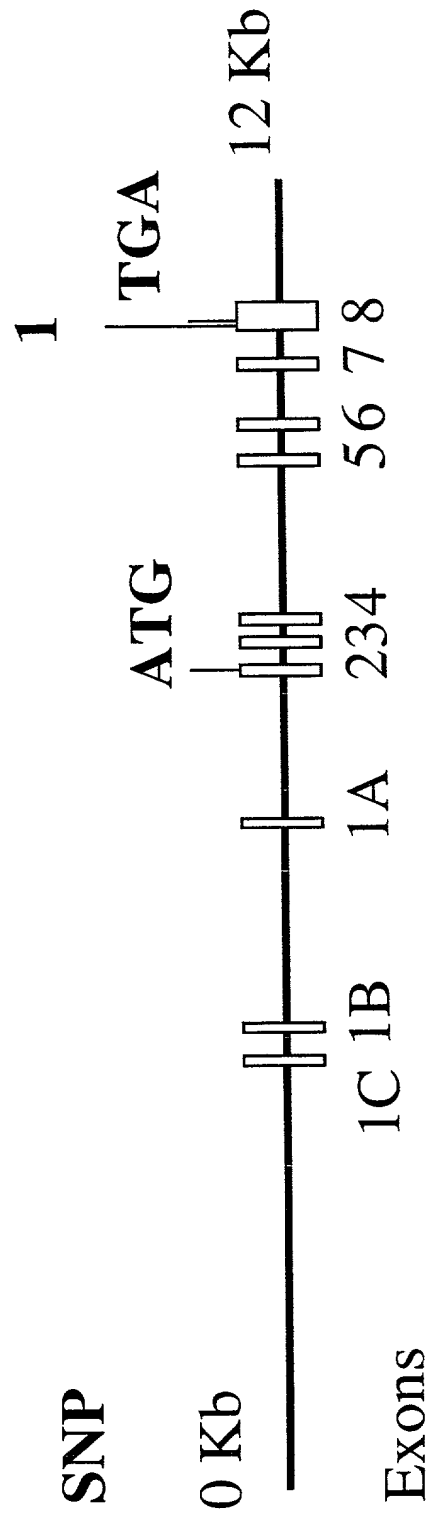


Fig. 235

Sulfotransferase 1C1 (*SULT1C1*)

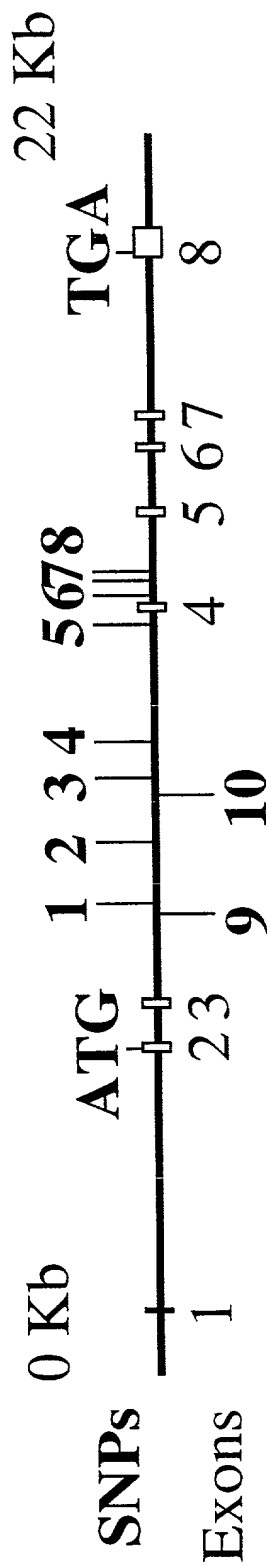
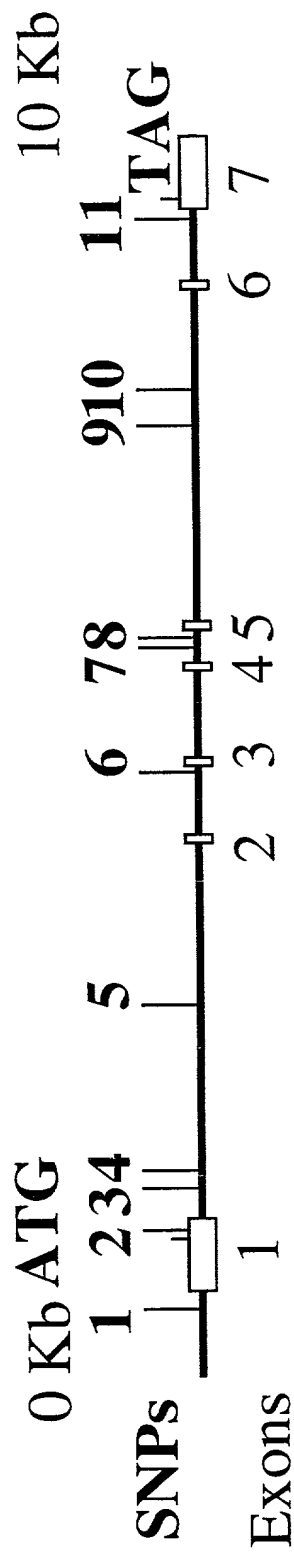
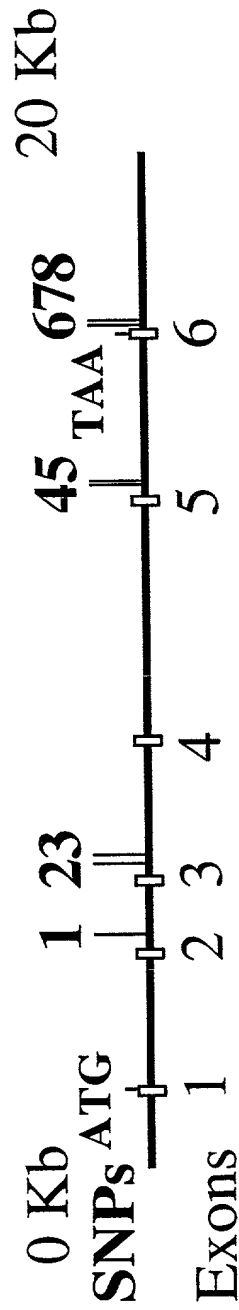


Fig. 236

Sulfotransferase 1C2 (*SULT1C2*)



*Fig. 237* Sulfotransferase 2A1 (*SULT2A1*)



*Fig. 238* Sulfotransferase 2B1 (*SULT2B1*)

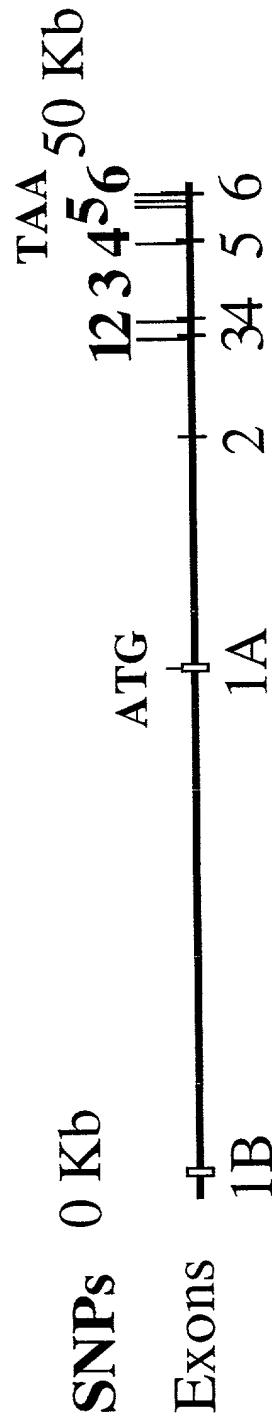


Fig. 239

Sulfotransferase-related protein 3 (*SULTX3*)

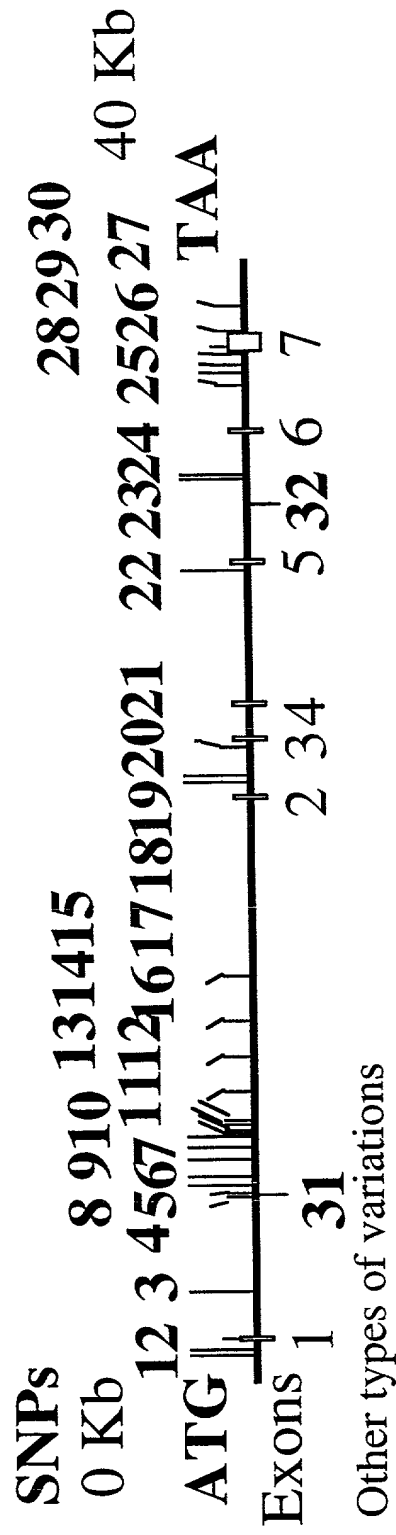


Fig. 240 Tyrosylprotein sulfotransferase 1 (*TPST1*)

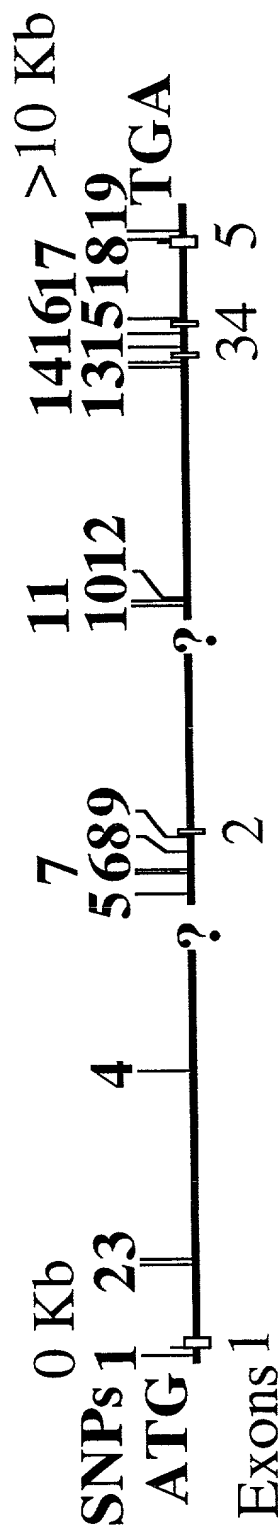


Fig. 241 Tyrosylprotein sulfotransferase 2 (*TPST2*)

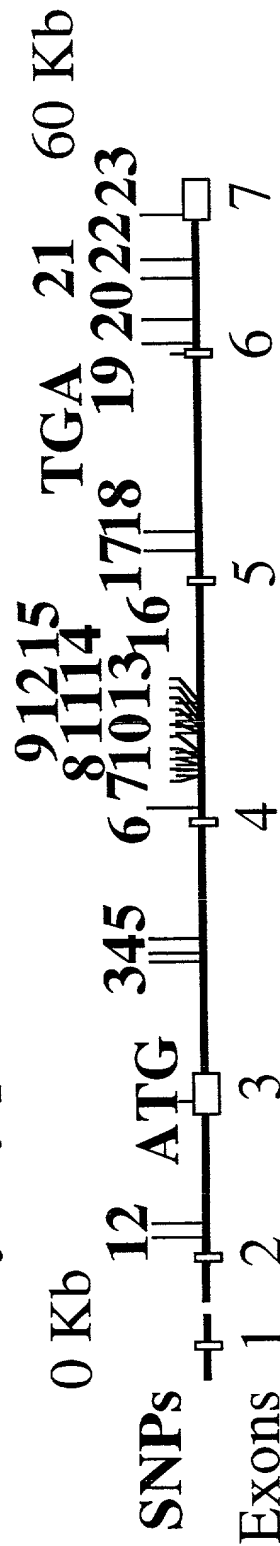




Fig. 242

# Cerebroside Sulfotransferase (*CST*)

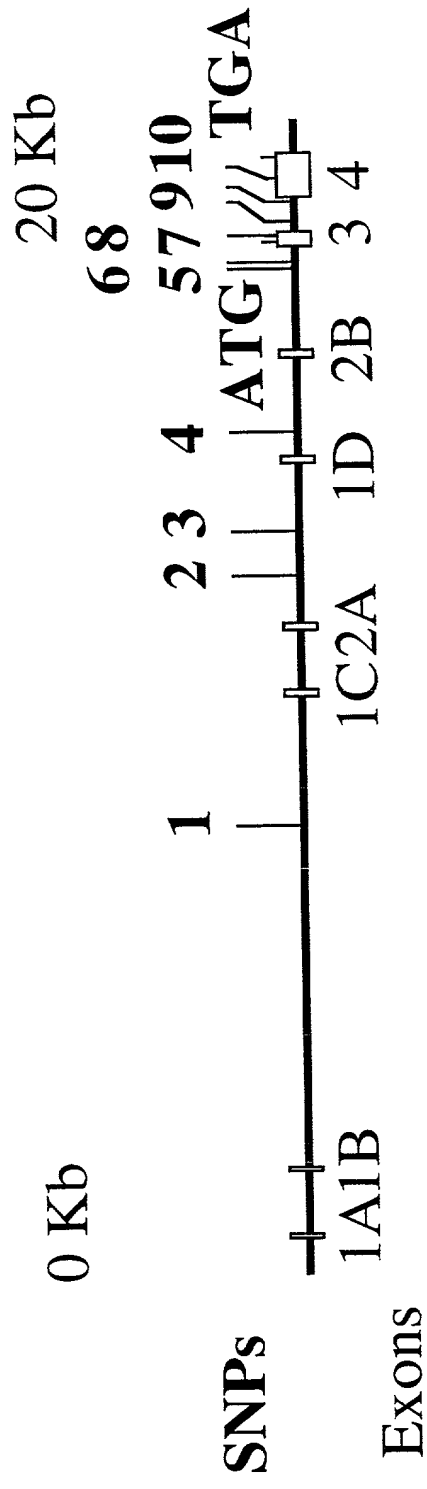


Fig. 243

# Thyroid hormone sulfotransferase (*ST1B2*)

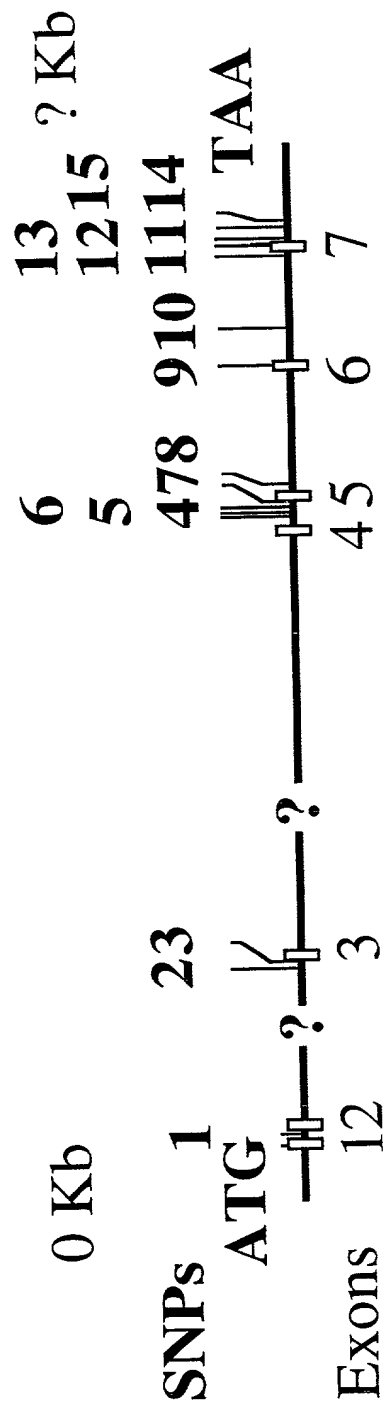




Fig. 245

# Carbohydrate sulfotransferase 2 (*CHST2*)

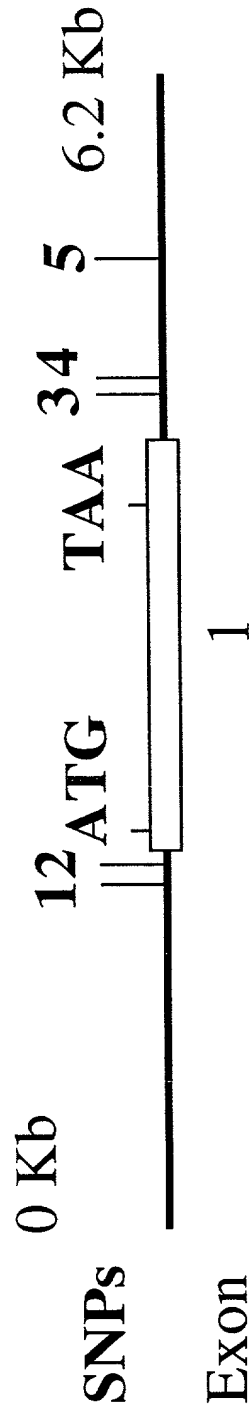




Fig. 247

# Carbohydrate sulfotransferase 4 (*CHST4*)

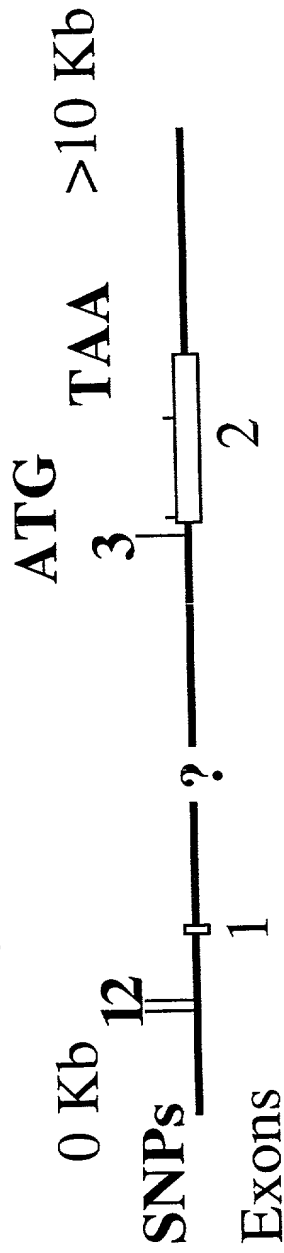


Fig. 248

# Carbohydrate sulfotransferase 5 (*CHST5*)

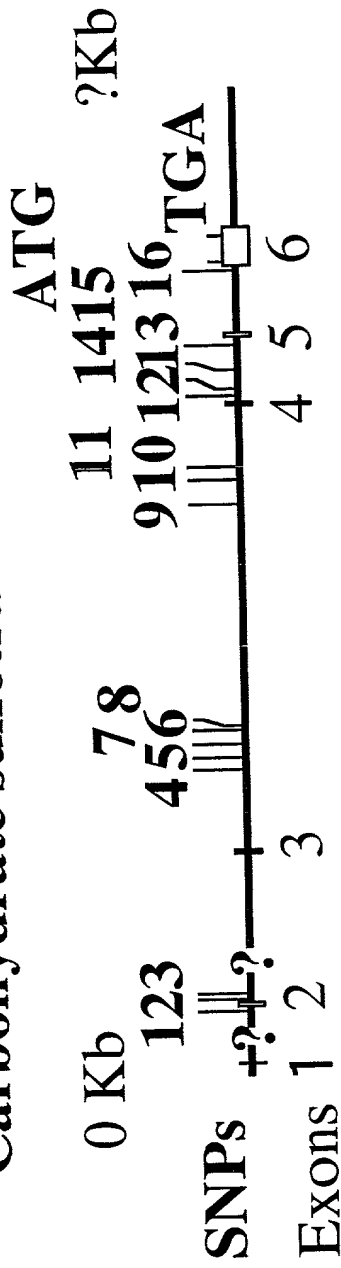


Fig. 249

# HNK-sulfotransferase (*HNK-1ST*)

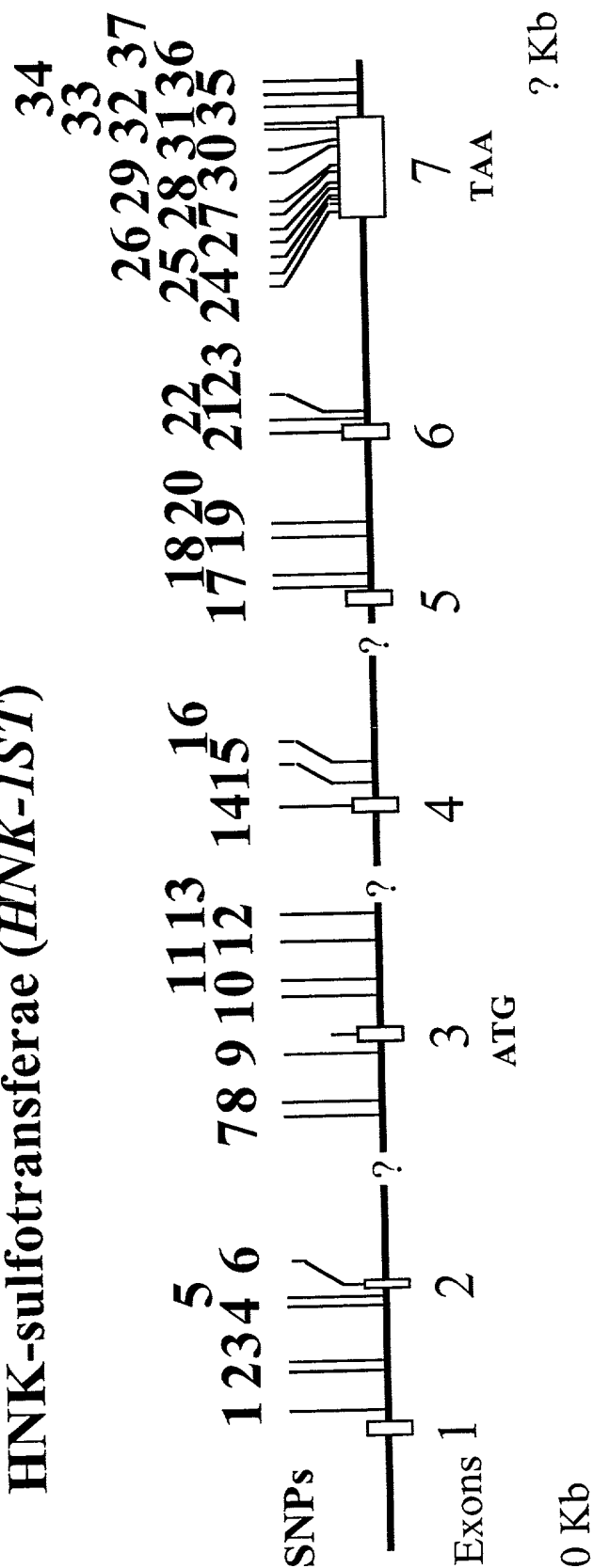


Fig. 250

# Estrogen sulfotransferase (*STE*)

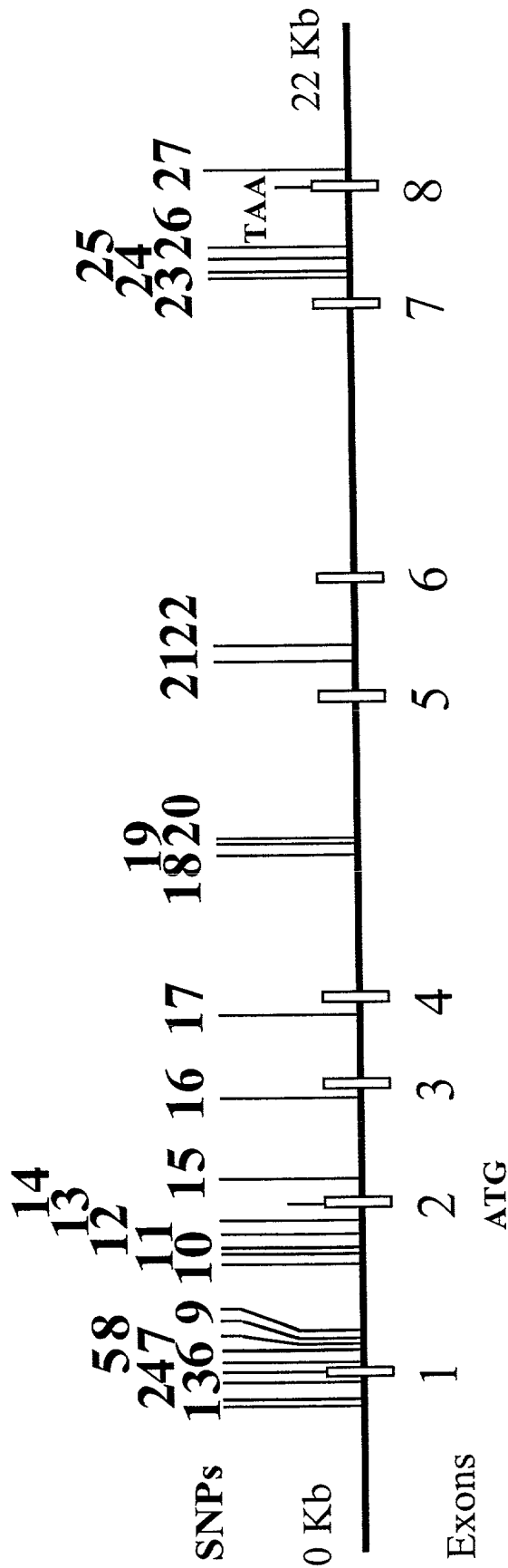




Fig. 251 NAD(P)H:quinone oxidoreductase 1 (*NQO1*)

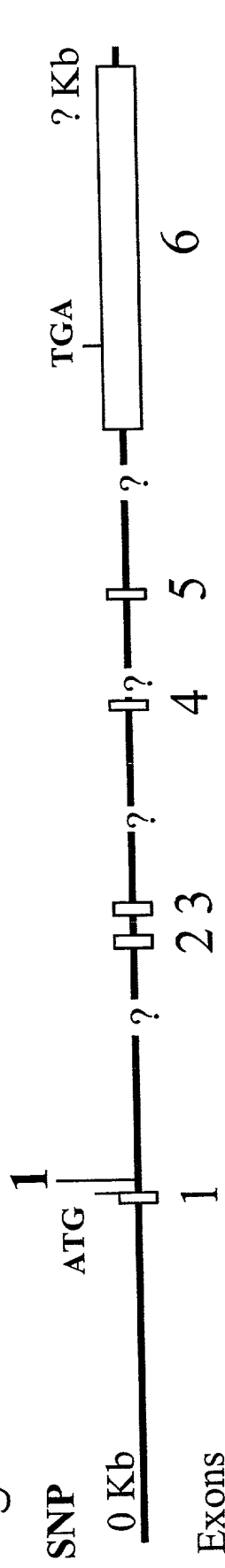


Fig. 252 NRH:quinone oxidoreductase 2 (*NQO2*)

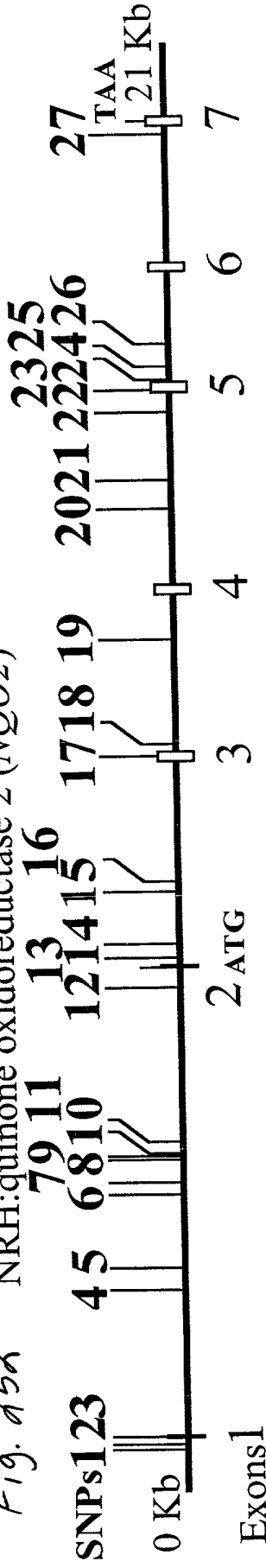


Fig. 253 p53-induced gene 3 (*PIG3*) / Quinone oxidoreductase homolog

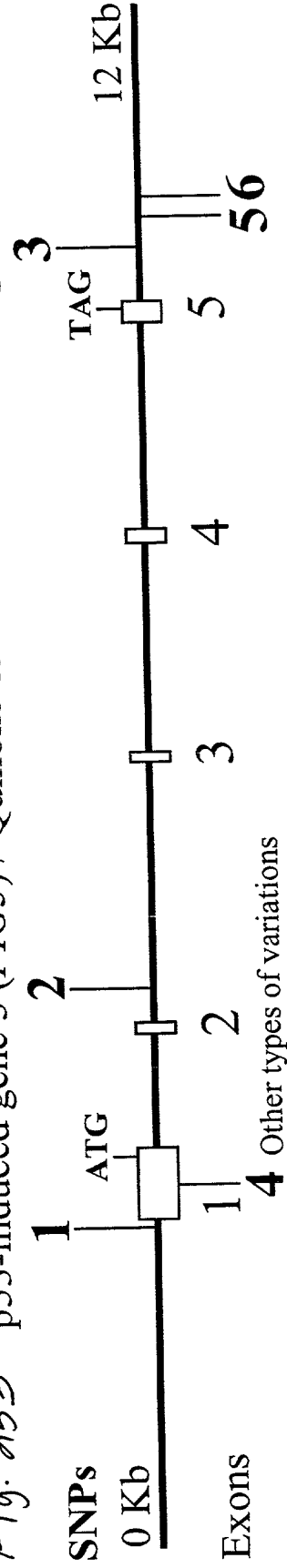


Fig. 254 NADH ubiquinone oxidoreductase 1 alpha subcomplex 1 (*NDUF41*)

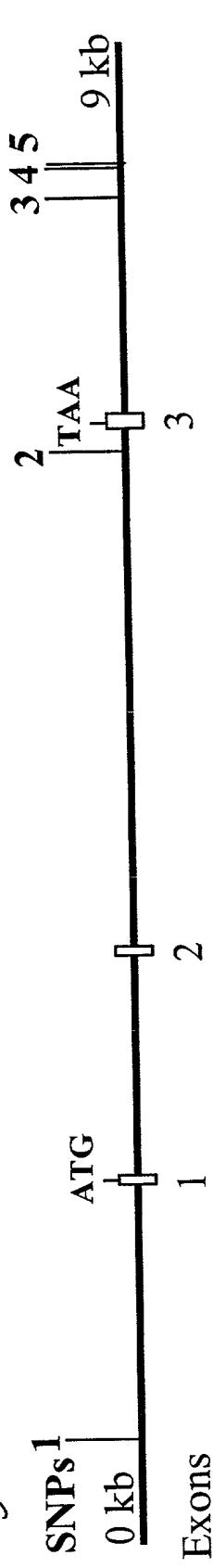


Fig. 255 NADH ubiquinone oxidoreductase 1 alpha subcomplex 2 (*NDUF42*)

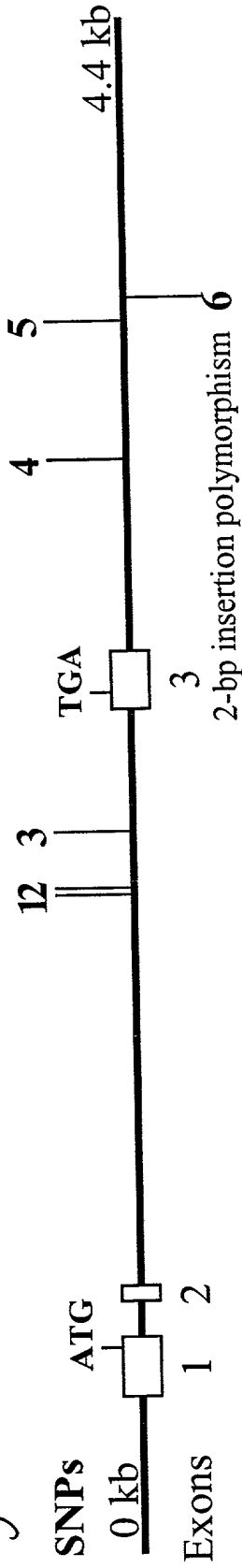
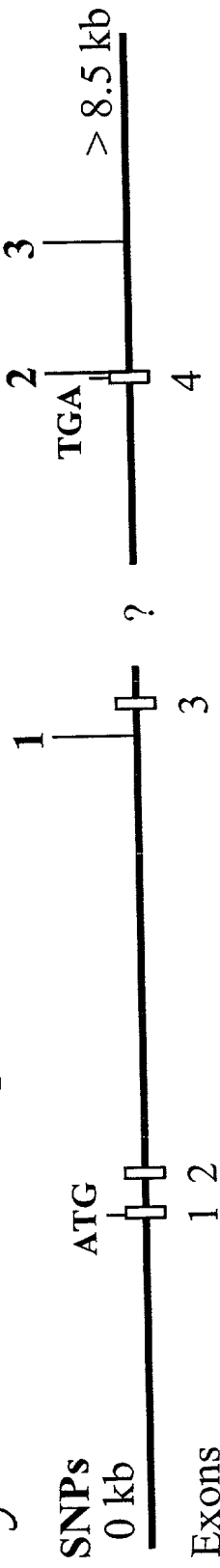


Fig. 256 NADH ubiquinone oxidoreductase 1 alpha subcomplex 3 (*NDUF43*)



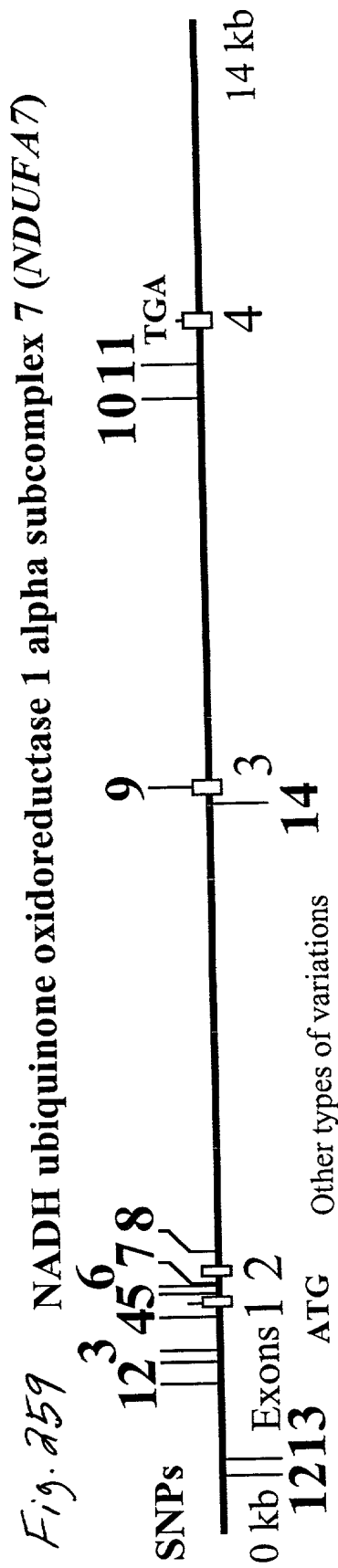
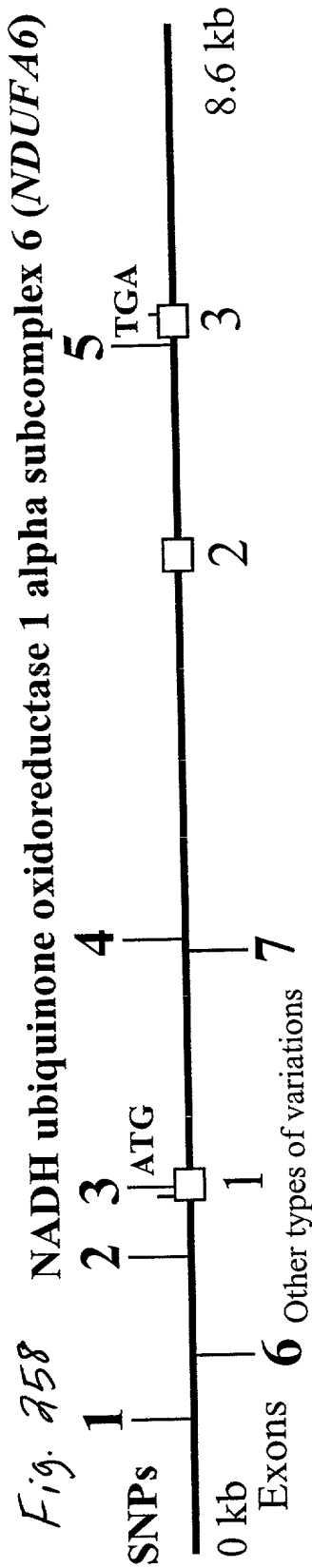
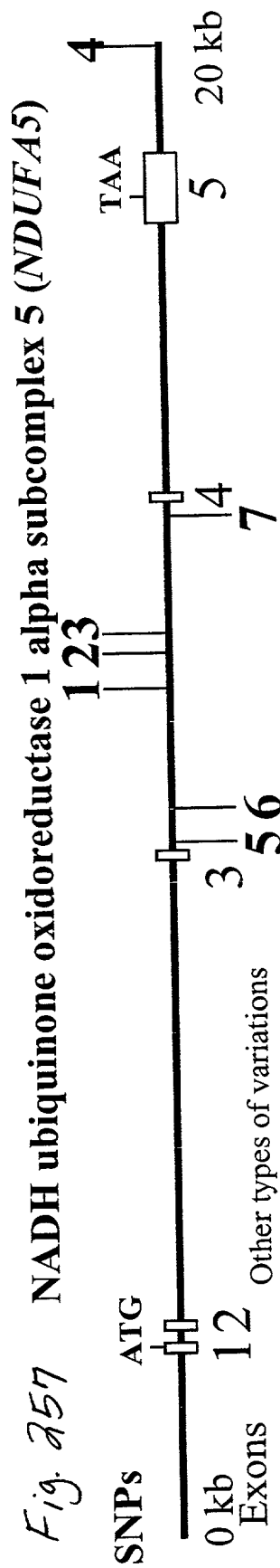


Fig. 260

# NADH ubiquinone oxidoreductase 1 alpha subcomplex 8 (*NDUF48*)

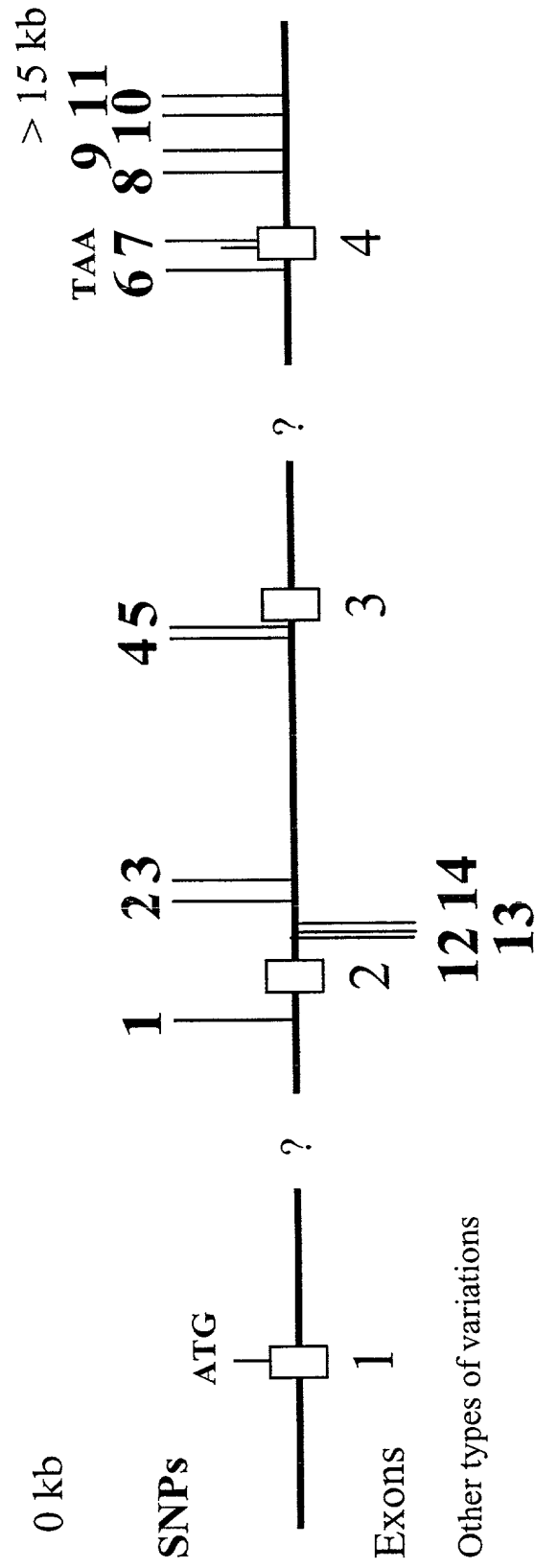


Fig. 261

# NADH ubiquinone oxidoreductase 1 alpha subcomplex 9 (*NDUF A9*)

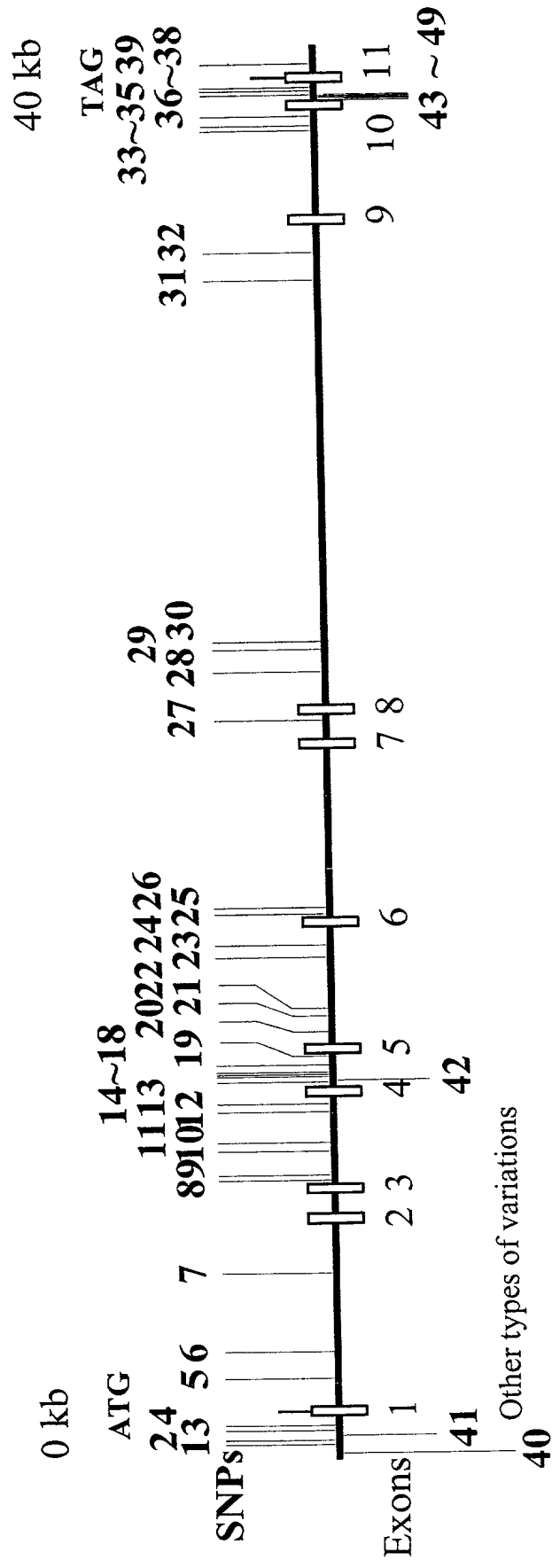
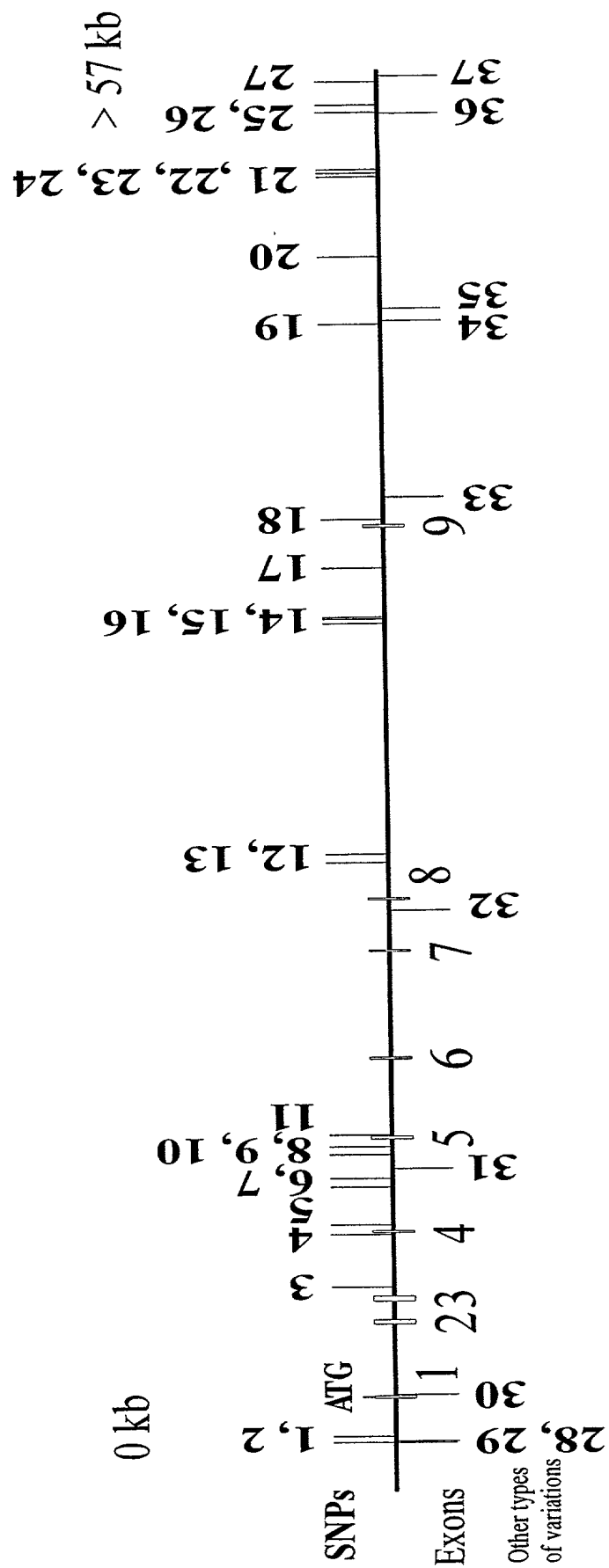


Fig. 262

NADH: ubiquinone oxidoreductase A 10 (NDUFA10)



*Fig. 263*  
**NADH ubiquinone oxidoreductase 1 alpha/beta subcomplex 1**  
**(*NDUFAB1*)**

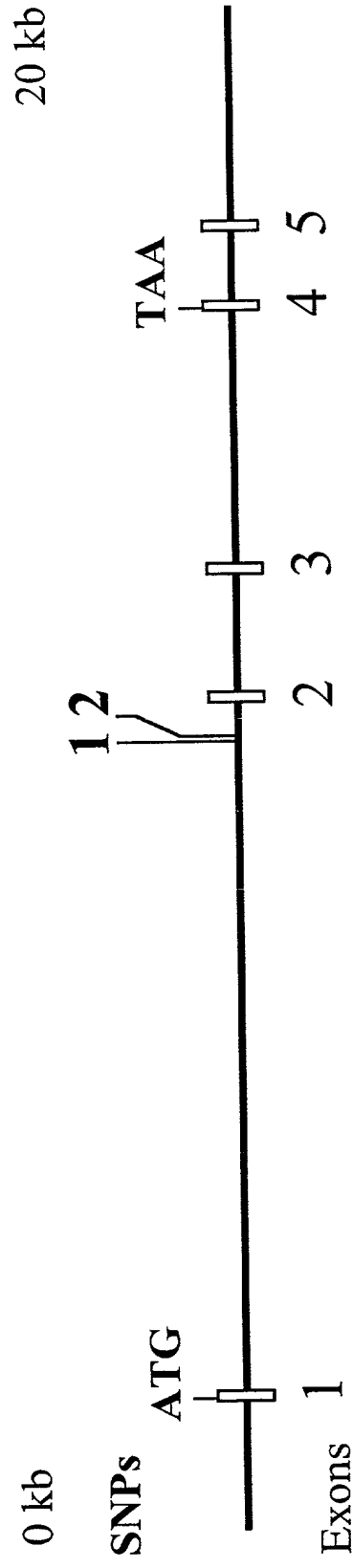


Fig. 264

NADH ubiquinone oxidoreductase 1 beta subcomplex 3 (*NDUFB3*)

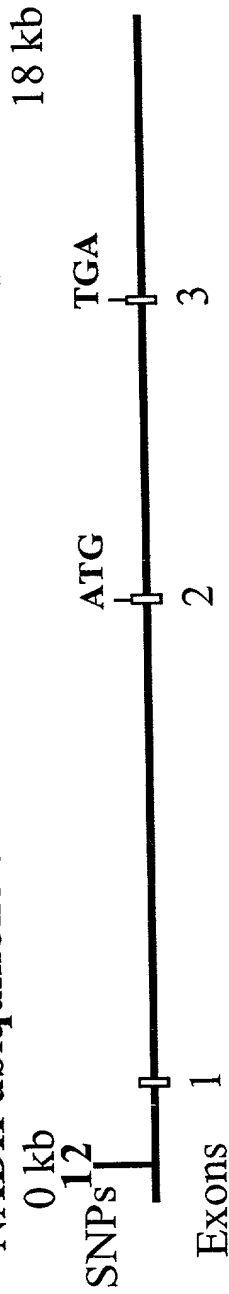


Fig. 265

NADH ubiquinone oxidoreductase 1 beta subcomplex 5 (*NDUFB5*)

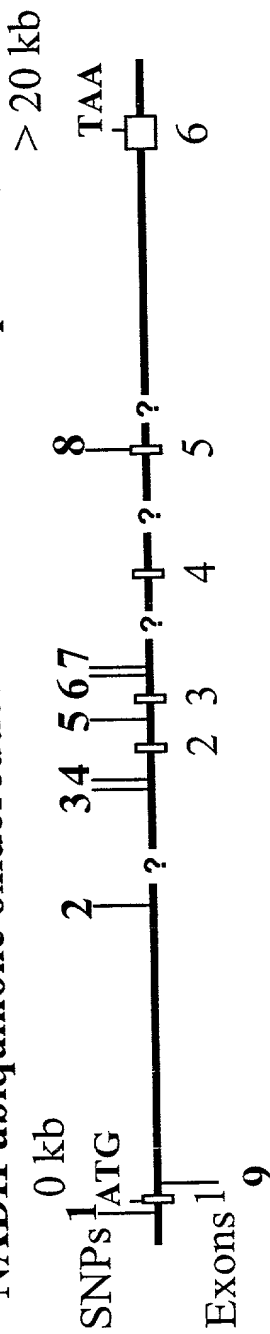


Fig. 266

NADH ubiquinone oxidoreductase 1 beta 7 (*NDUFB7*)

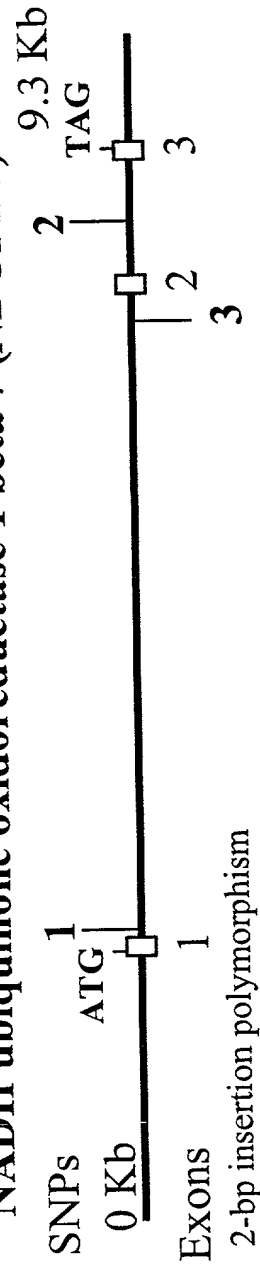






Fig. 270 NADH ubiquinone oxidoreductase Fe-S protein 5 (*NDUFS5*)

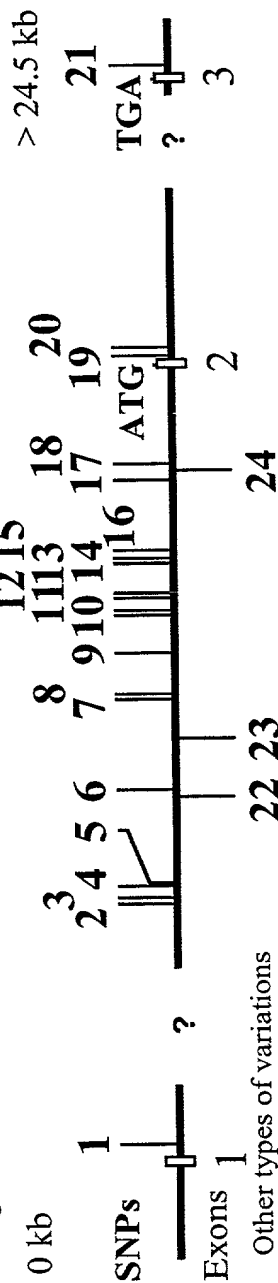


Fig. 271 NADH ubiquinone oxidoreductase Fe-S protein 6 (*NDUFS6*)

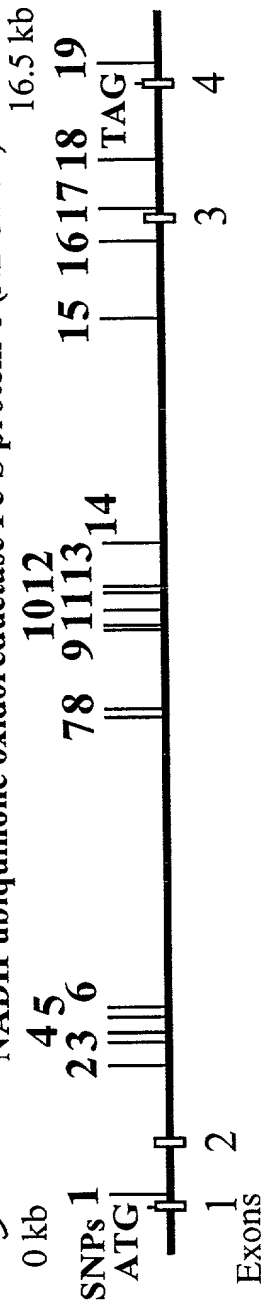


Fig. 272 NADH ubiquinone oxidoreductase Fe-S protein 8 (*NDUFS8*)

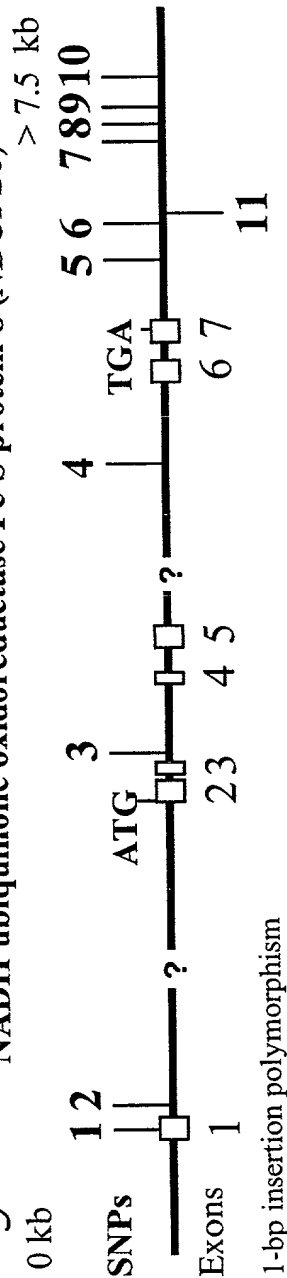


Fig. 273

NADH: ubiquinone dehydrogenase flavoprotein 1 (*NDUFV1*)

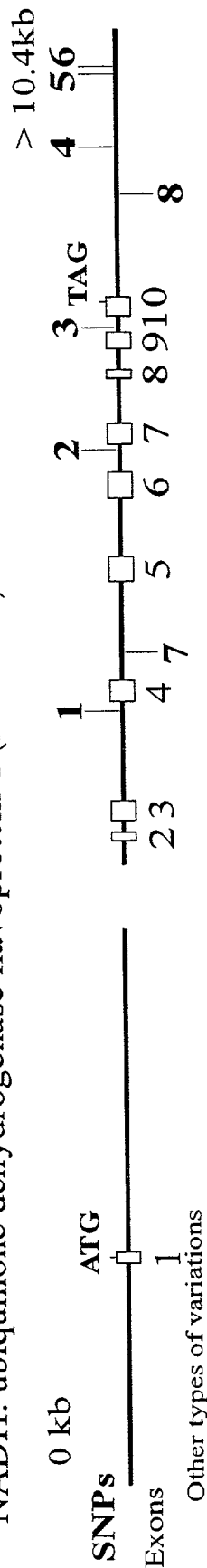


Fig. 274

NADH: ubiquinone oxidoreductase flavoprotein 2 (*NDUFV2*)

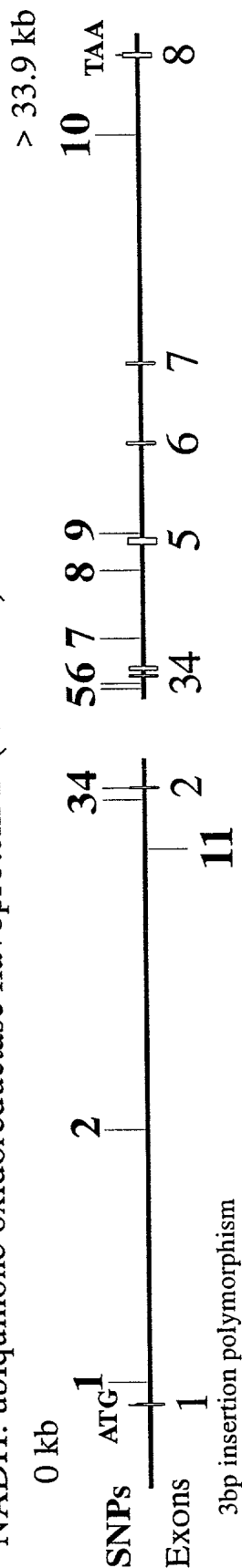


Fig. 275

NADH: ubiquinone oxidoreductase flavoprotein 3 (*NDUFV3*)

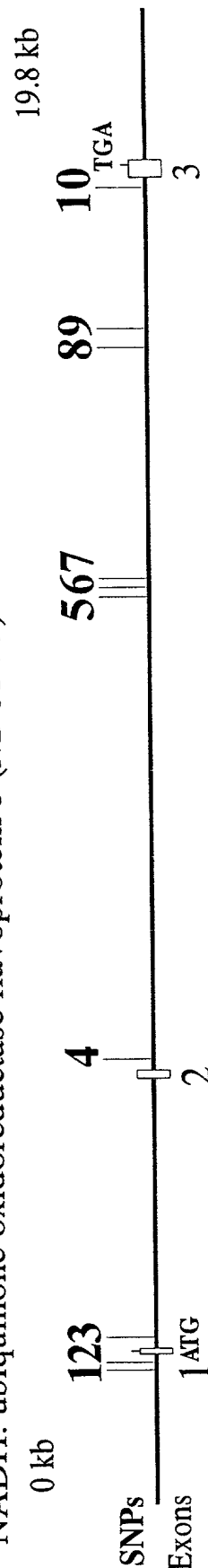


Fig. 276

*Gamma- glutamyltransferase 1 ( GGT1 )*

ACCESSION D87002.1

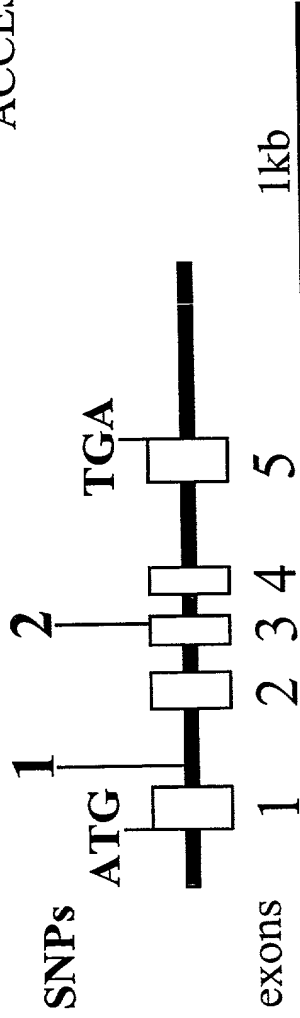


Fig. 277

*Transglutaminase 1 (TGMI)*

ACCESSION M98447.1

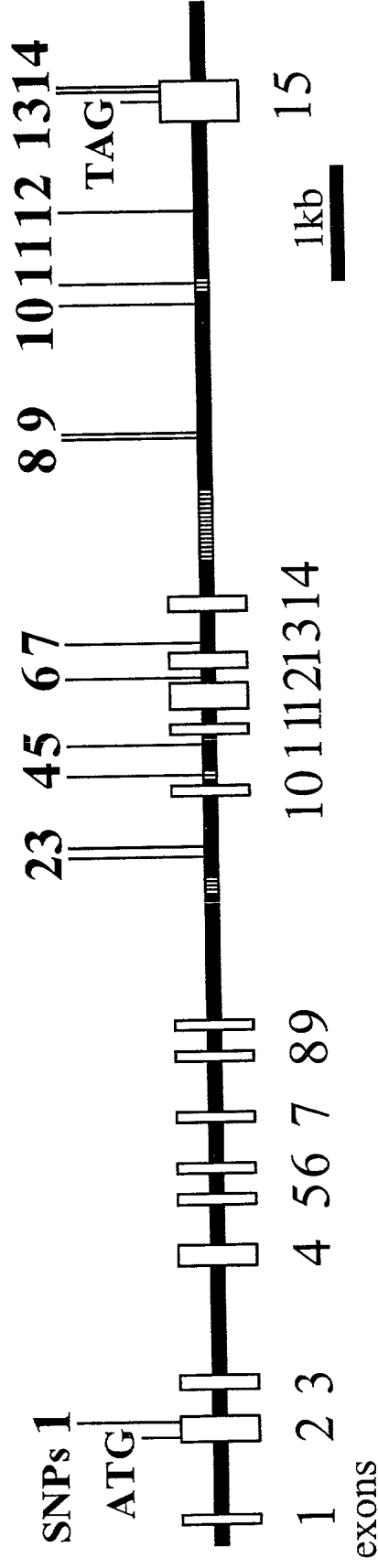


Fig. 278

Cytochrome P450, subfamily I, polypeptide 1 (*CYP1A1*)

ACCESSION X04300.1 AC020705.4

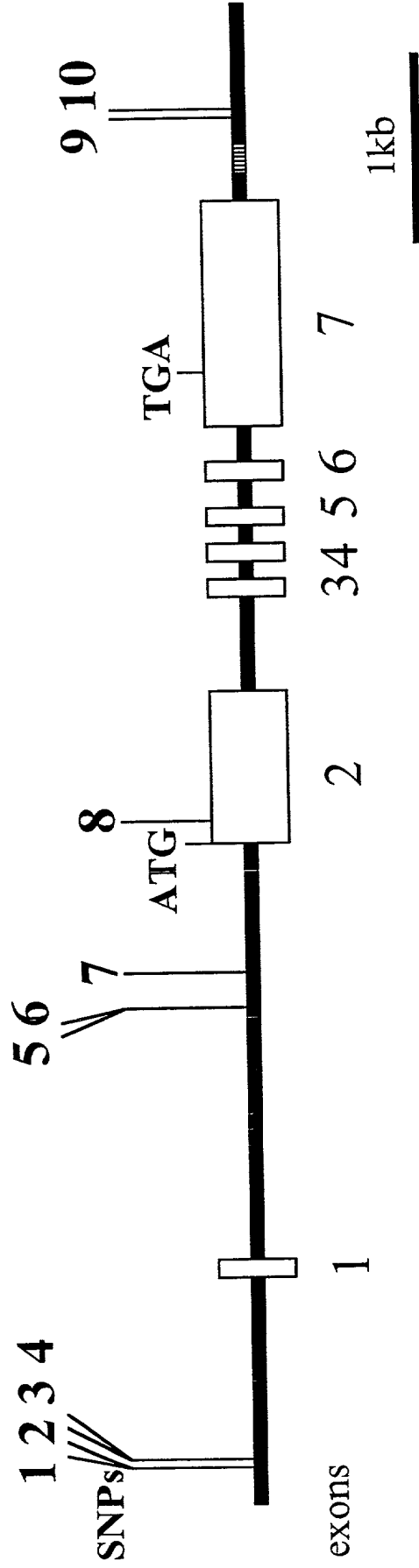


Fig. 279

Cytochrome P450, subfamily 1, polypeptide 2 (CYP1A2)

ACCESSION AC020705.4

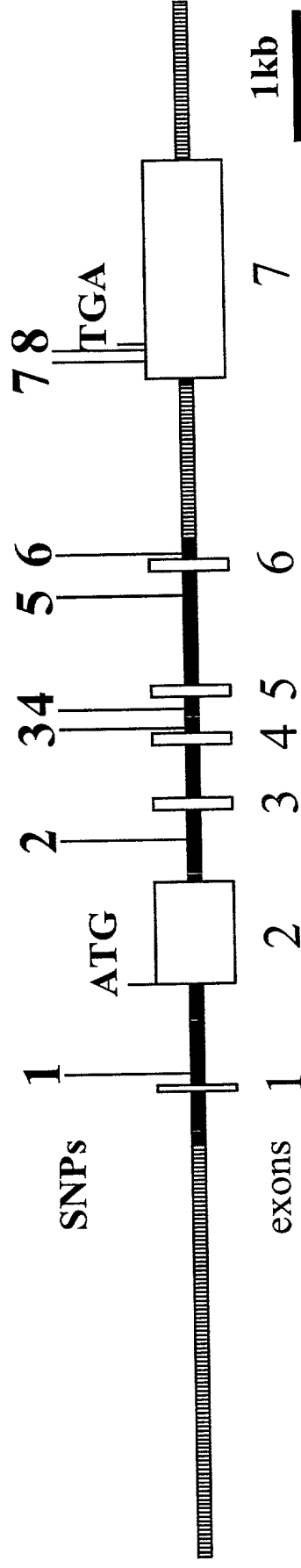


Fig. 280

Cytochrome P450, subfamily 1, polypeptide 1 (CYP1B1)

ACCESSION AC009229.4

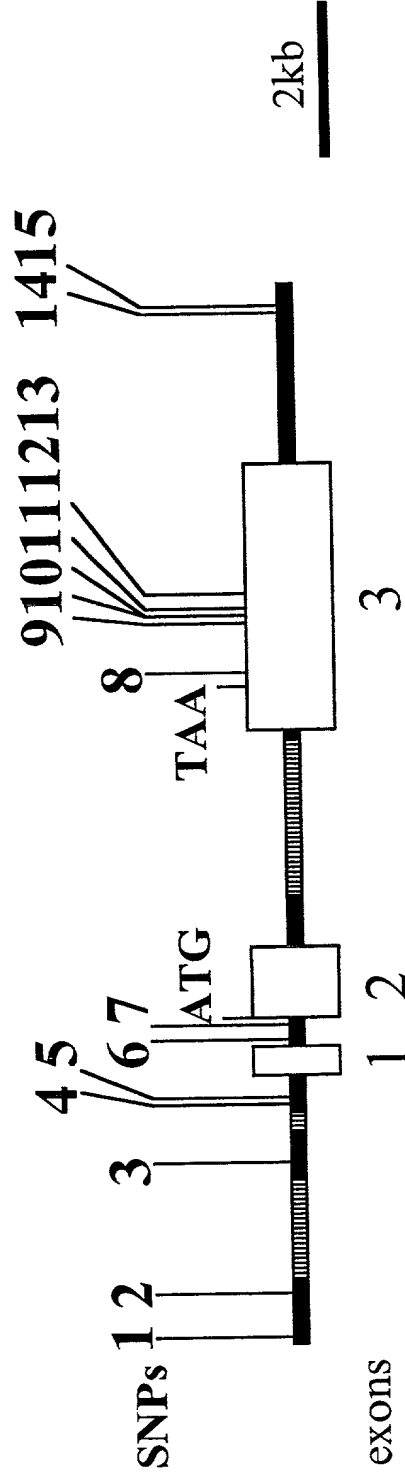


Fig. 281  
*Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)*

ACCESSION AF280107.1

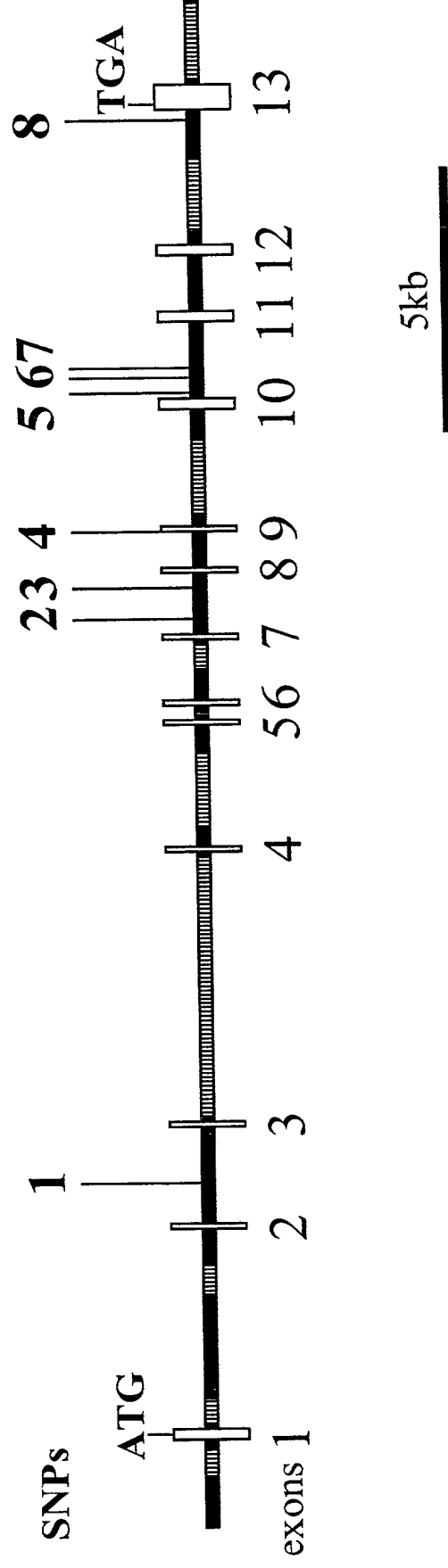


Fig. 282

Cytochrome P450, subfamily IIIA, polypeptide 5 (CYP3A5)

ACCESSION AC005020.5

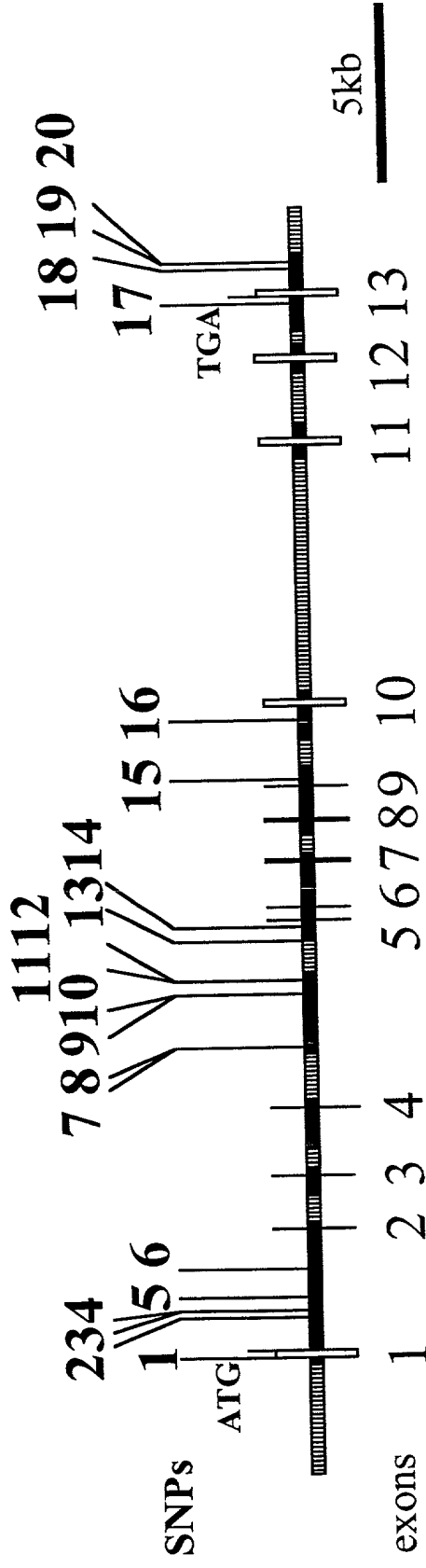


Fig. 283

Cytochrome P450, subfamily IIIA, polypeptide 7 (CYP3A7)

ACCESSION AF280107.1

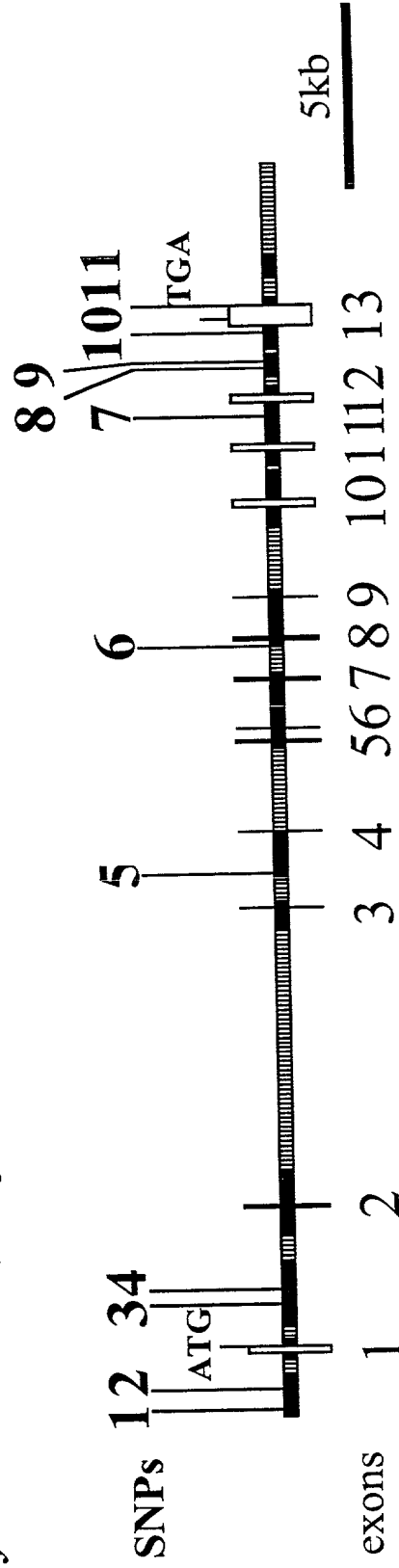




Fig. 784 Cytochrome P450, subfamily IIIA, polypeptide 43 (CYP3A43)

ACCESSION AC011904.3

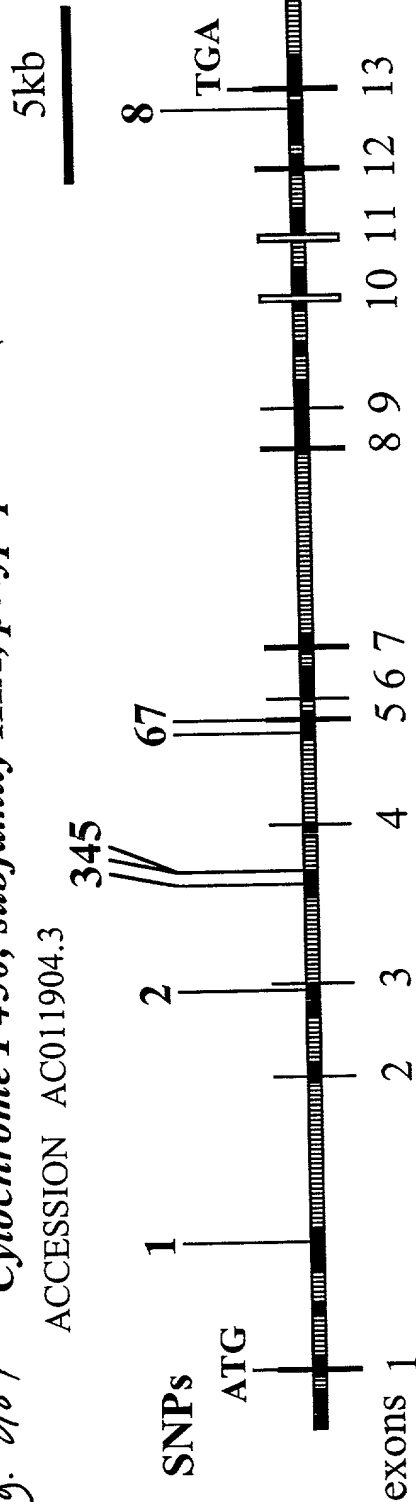


Fig. 785 Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)

ACCESSION AL356793.10

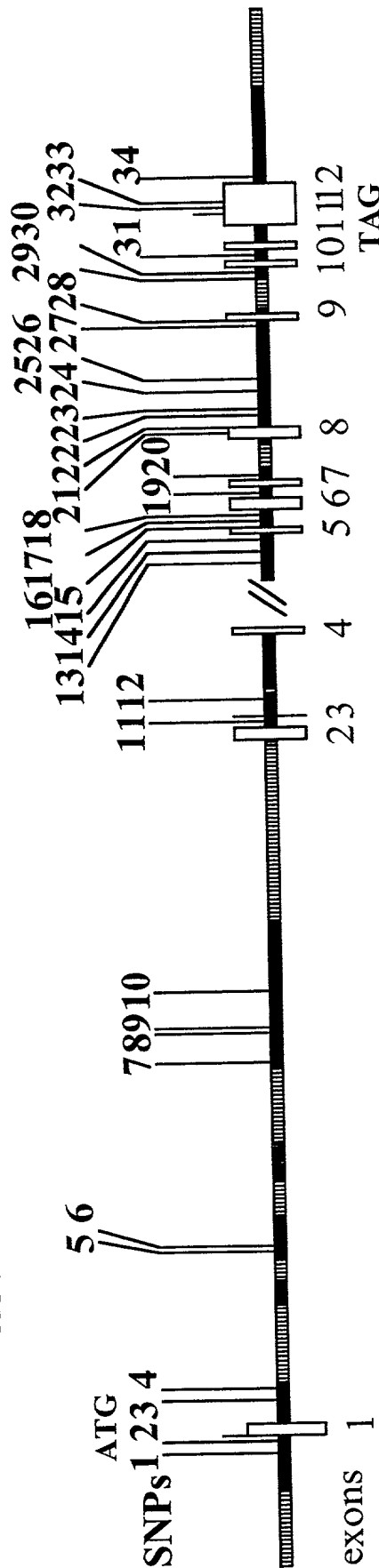


Fig. 286 Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2) ACCESSION AC005336.1

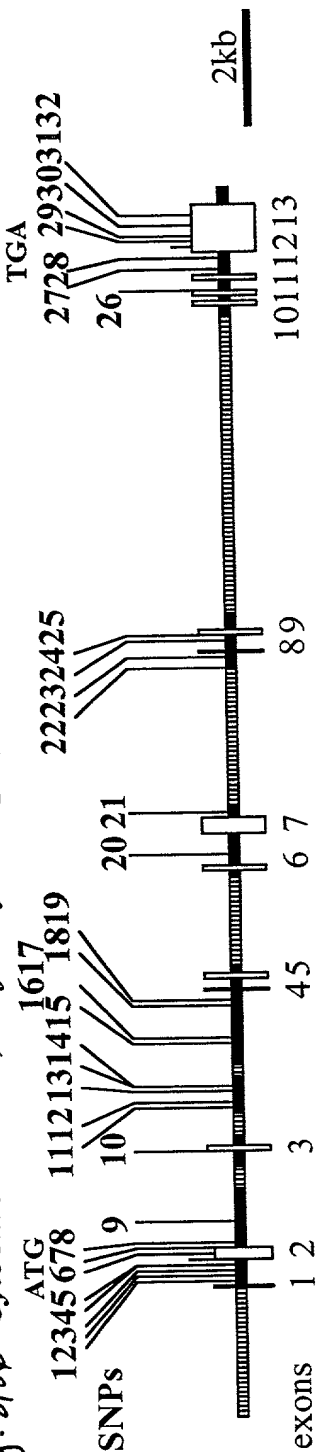


Fig. 287 Cytochrome P450, subfamily IVF, polypeptide 3 (CYP4F3) 2425262728 ACCESSION AD000685.1

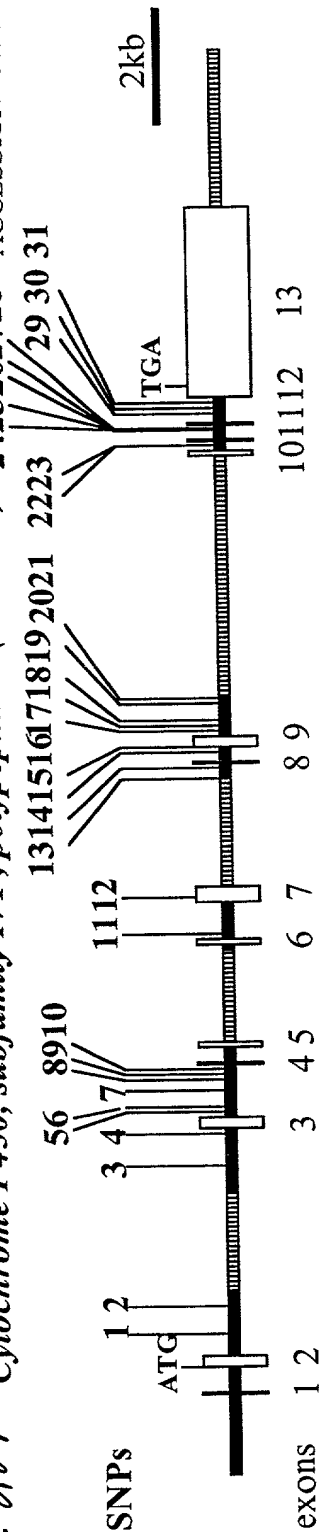


Fig. 288 Cytochrome P450, subfamily IVF, polypeptide 8 (CYP4F8) ACCESSION AC068845.3

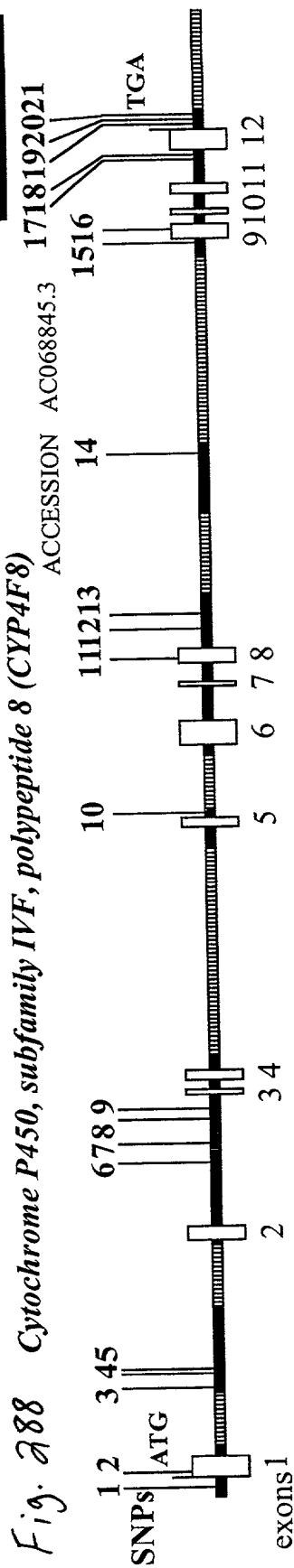


Fig. 289 Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)

ACCESSION AC009974.7

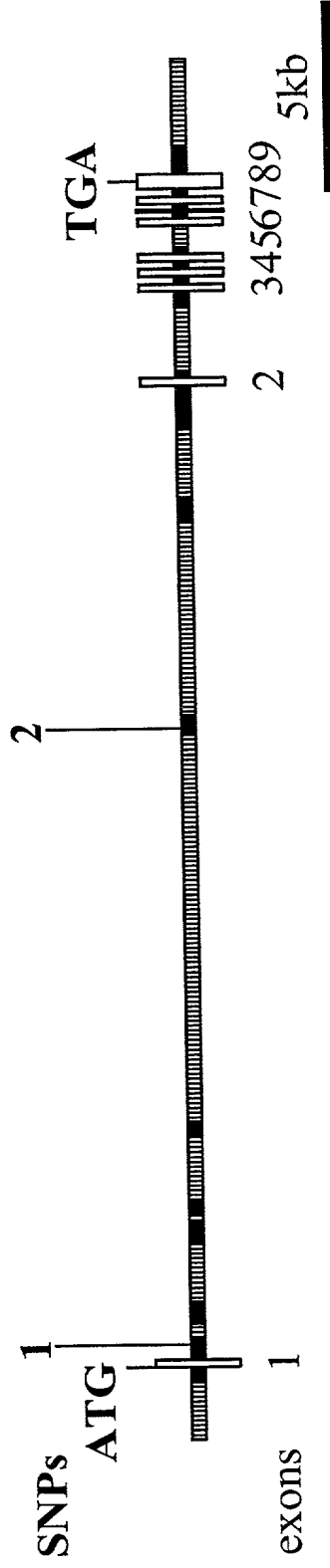


Fig. 290 Cytochrome P450, subfamily XXVIIIB, polypeptide 1 (CYP27B1)

ACCESSION AC025165.27

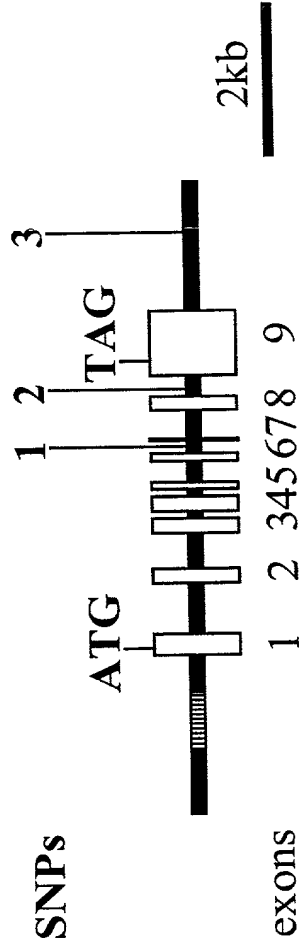


Fig. 291 Arylacetamide deacetylase (AADAC) AC068647.4

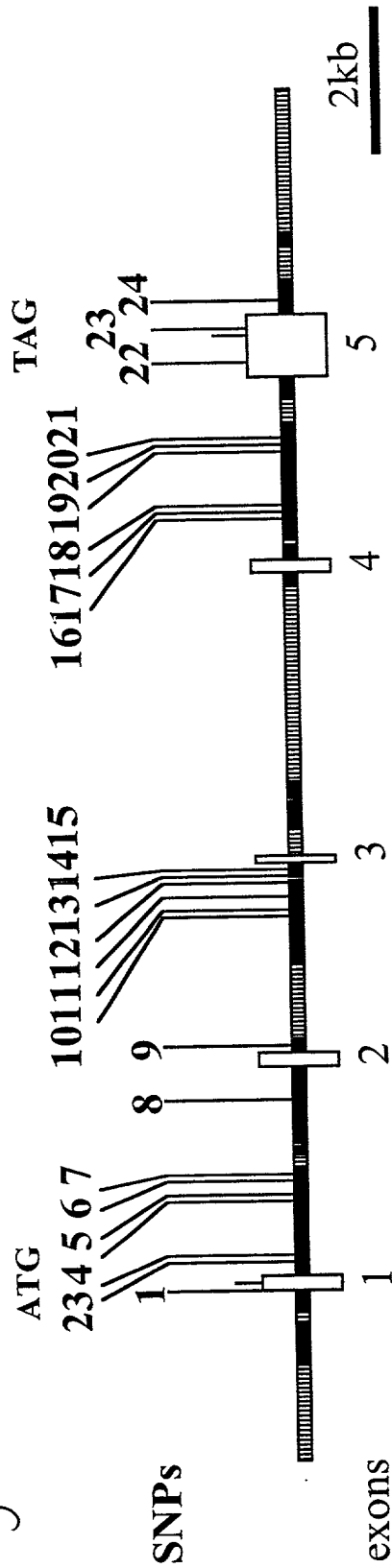
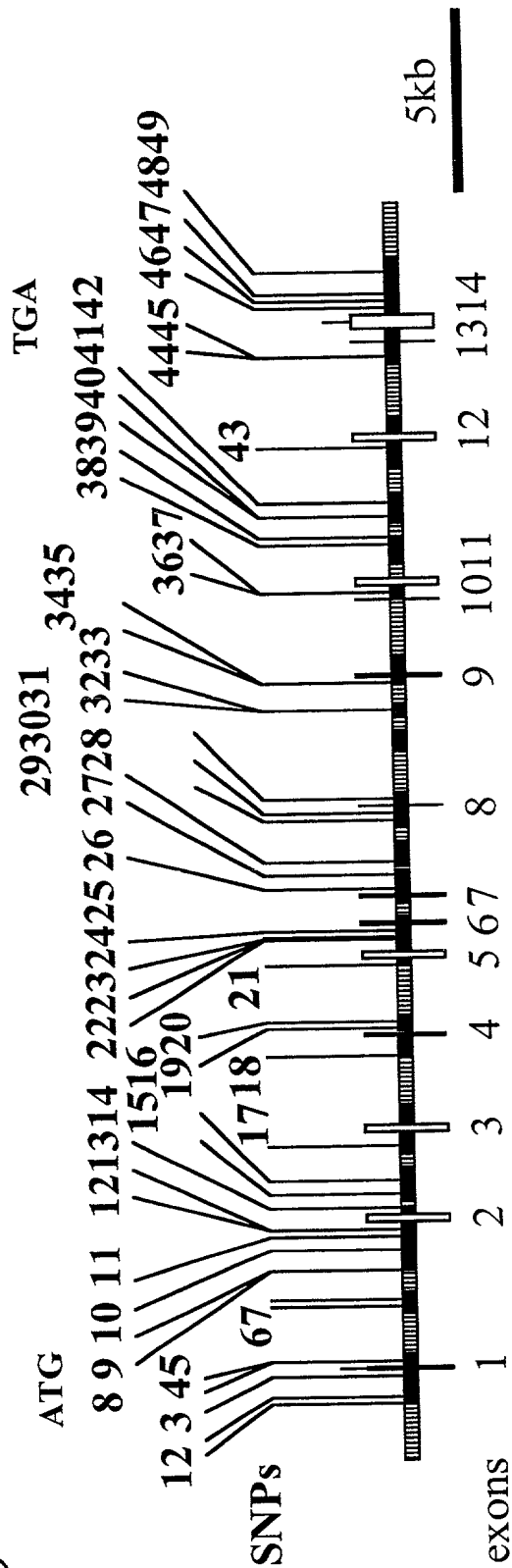


Fig. 292 Carboxylesterase 1 (CES1) AC007602.4



*Fig. 293*  
*Carboxylesterase 2 (CES2)*

ACCESSION AC027131.4

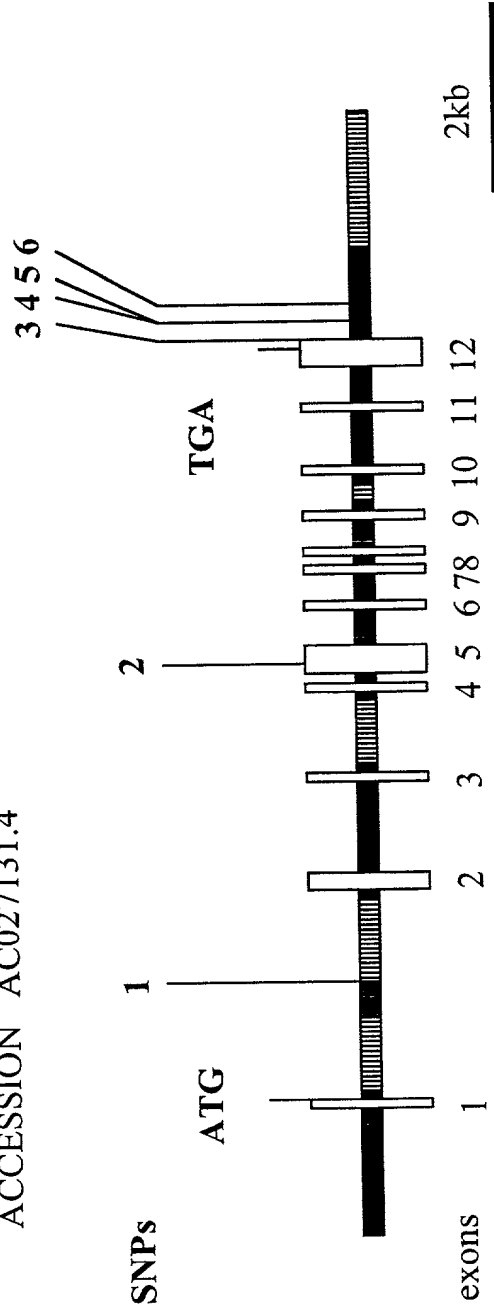


Fig. 294 *Granzyme A (GZMA)*

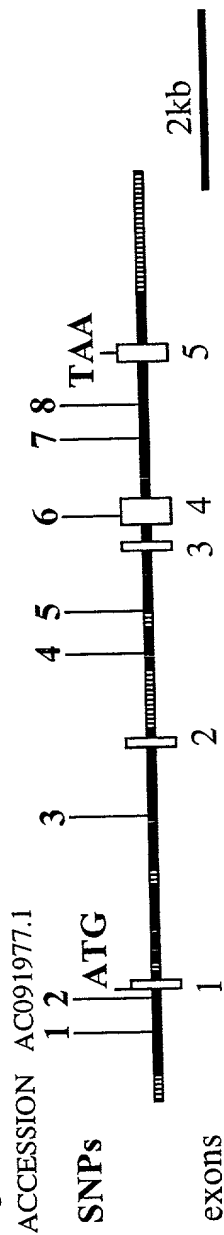


Fig. 295 *Granzyme B (GZMB)*

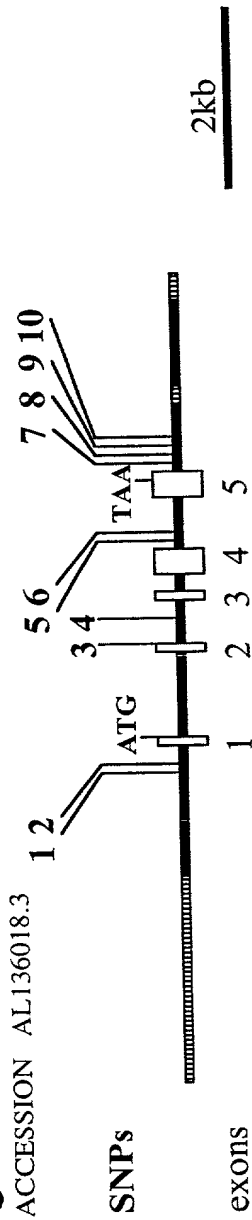


Fig. 296 *Esterase D (ESD)*

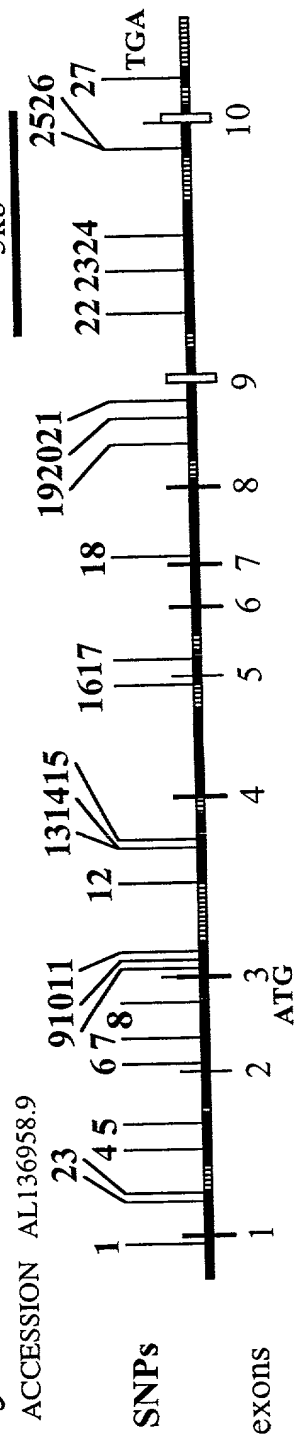


Fig. 297A *Carboxyl ester lipase (CEL)*  
 ACCESSION AL138750<sup>8</sup> AL162417.20 AF072711.1

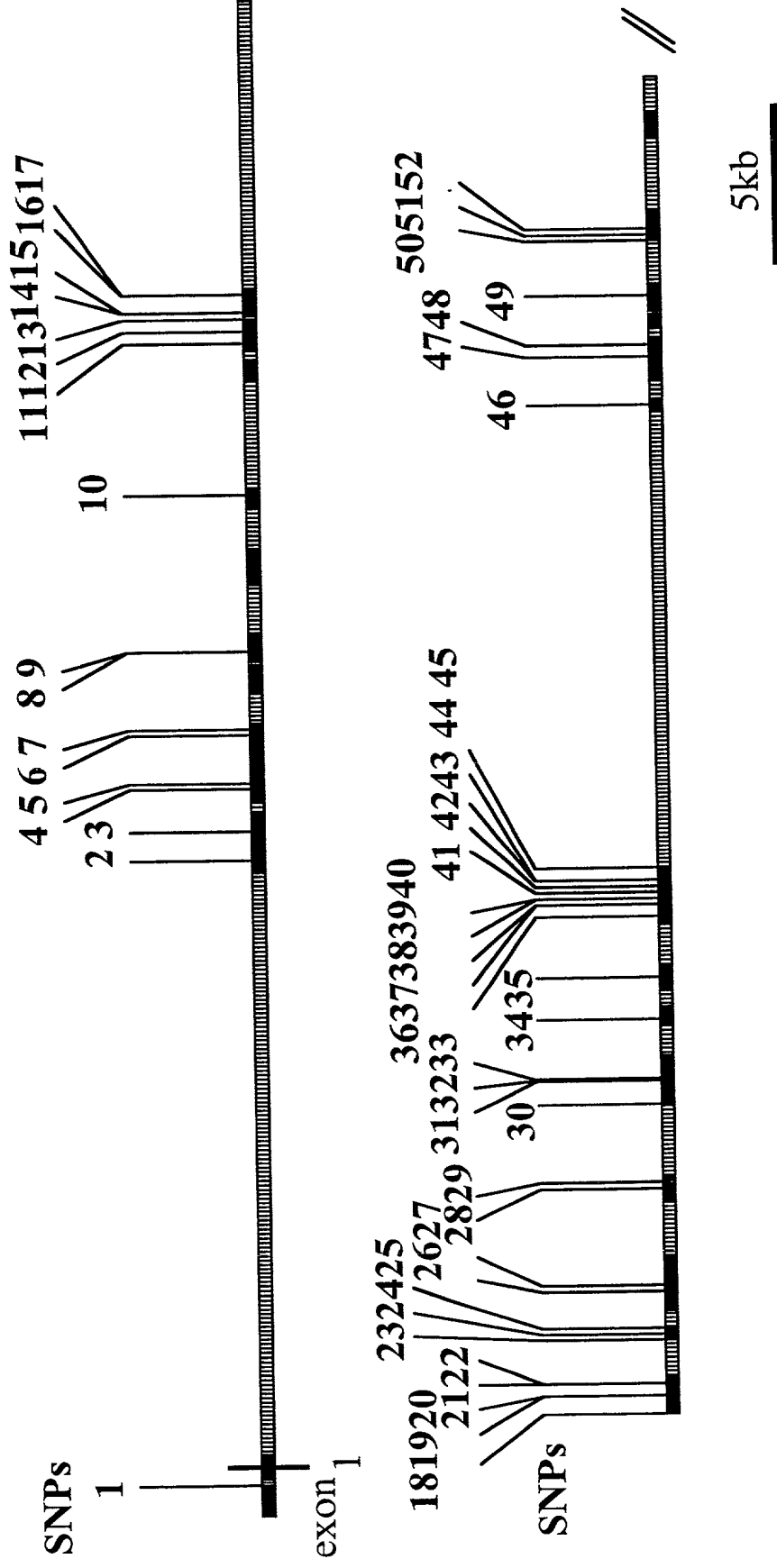


Fig. 297B

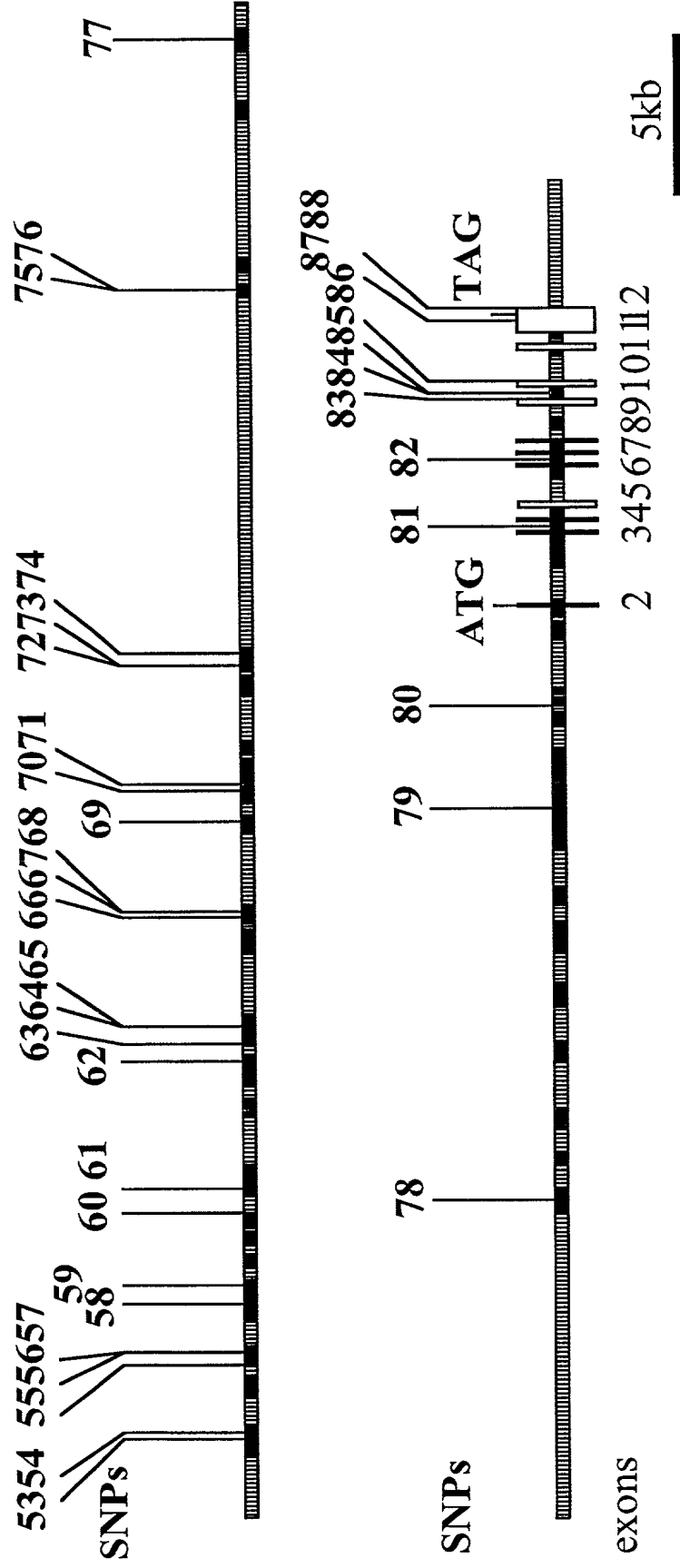




Fig. 798

Interleukin 17  
(cytotoxic T-lymphocyte-associated serine esterase 8) (IL17)

ACCESSION AL355513.11

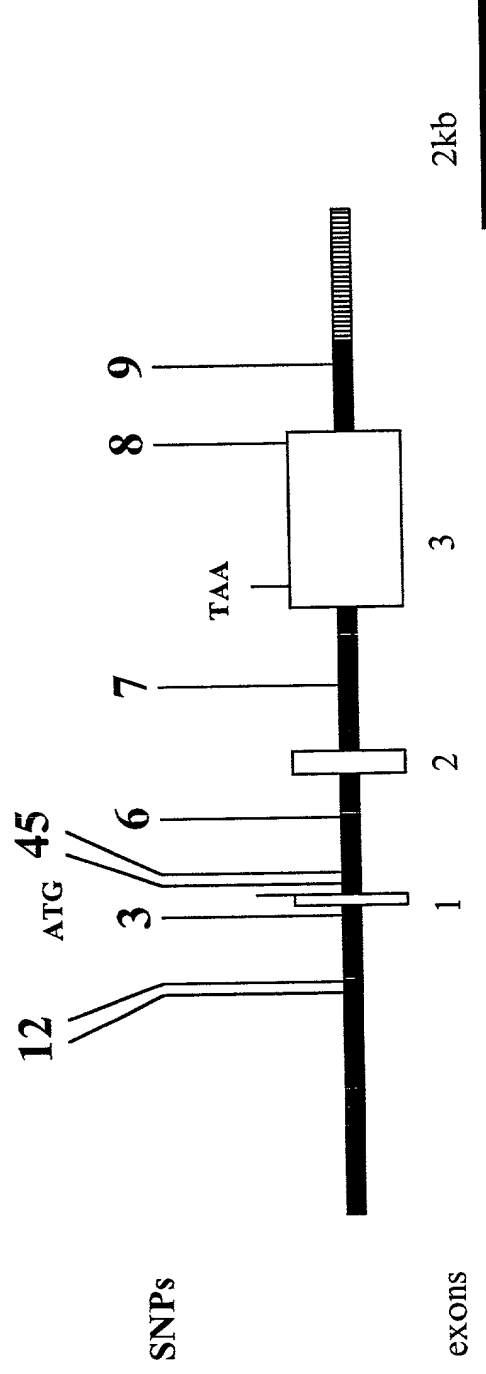


Fig. 299 *Ubiquitin carboxyl-terminal esterase L3 (UCHL3)*

ACCESSION AL137244.28

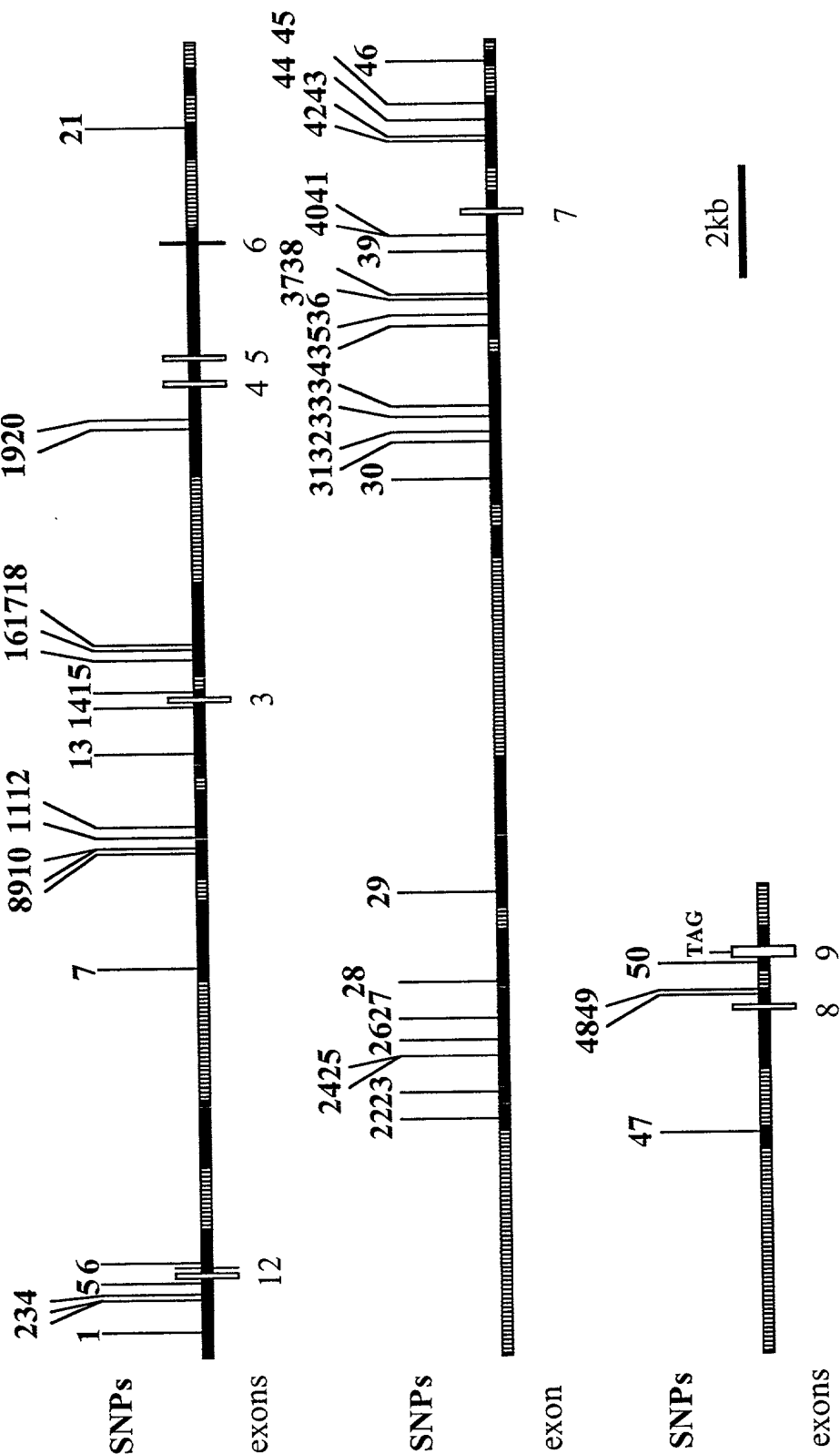
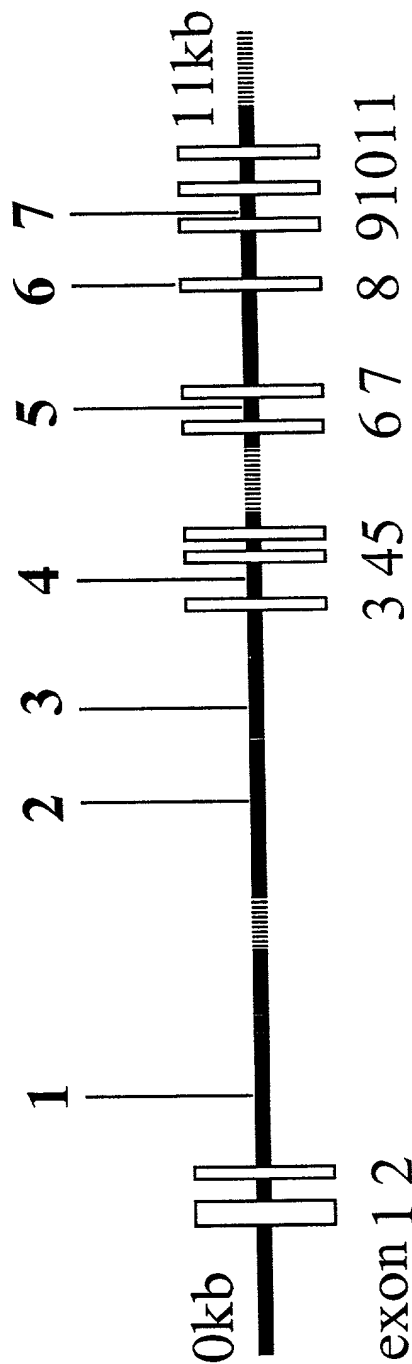


Fig. 300 *dolichyl-diphosphooligosaccharide-protein  
glycosyltransferase (DDOST)*

Accession No. D89060



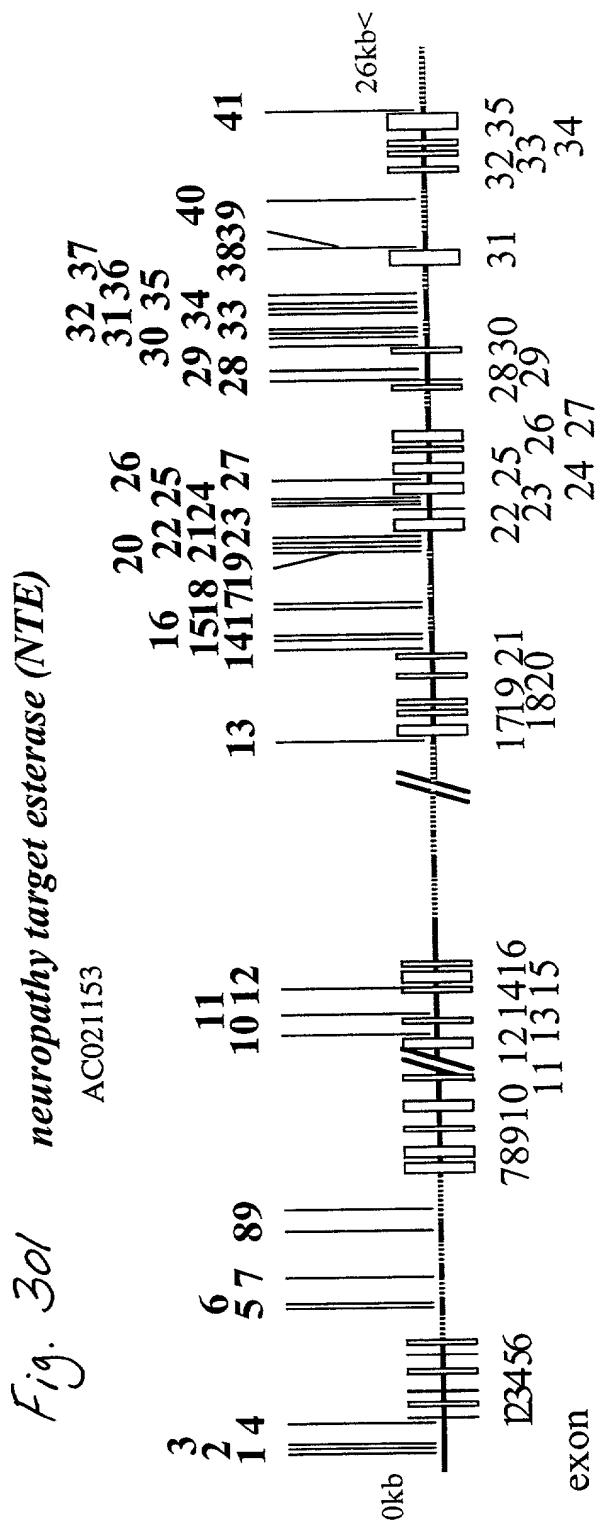


Fig. 302

*L1 cell adhesion molecule (L1CAM)*

Accession No. U52112

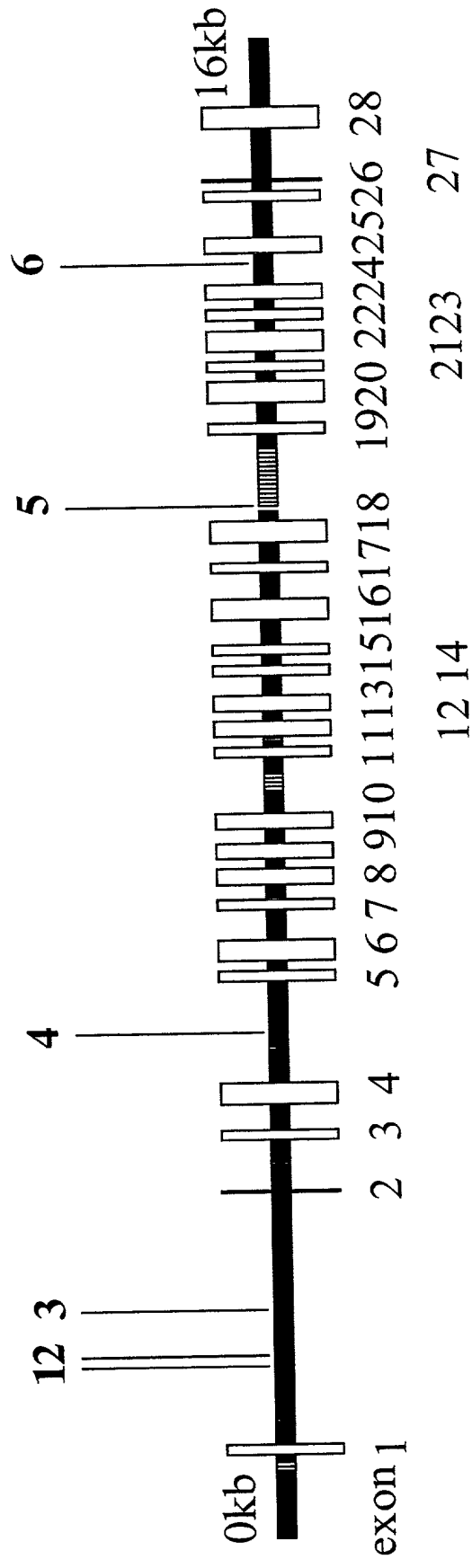


Fig. 303

*arylalkylamine N-acetyltransferase(AANAT)*

Accession No. U40391

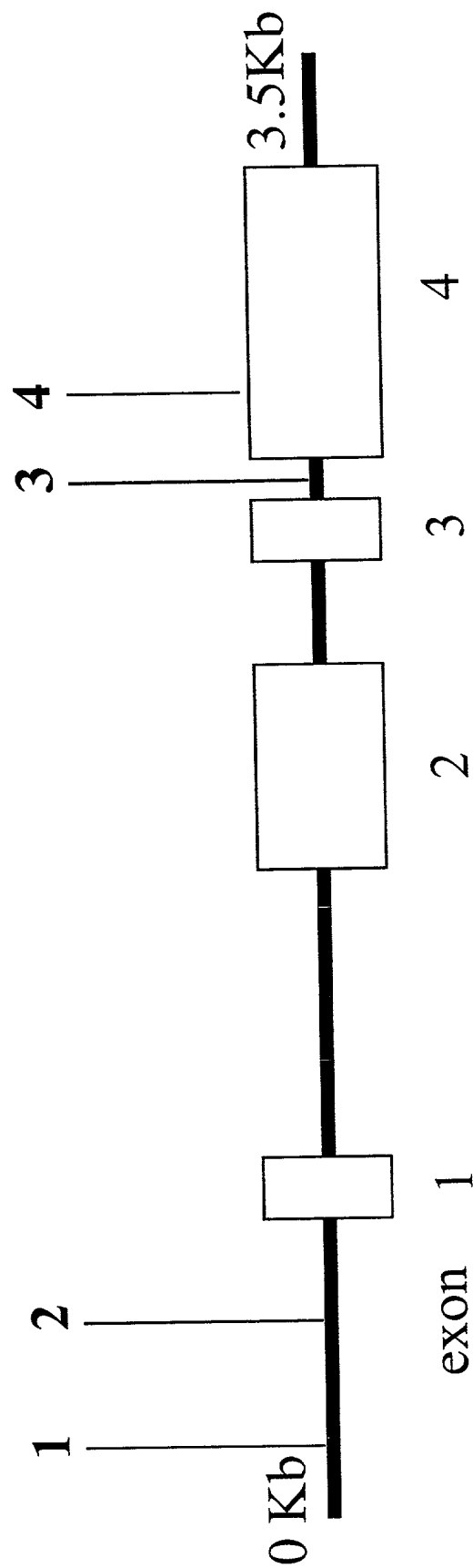


Fig. 304

*N*-acetyltransferase, homolog of *S. cerevisiae* (*ARD1*)

Accession No. U52112

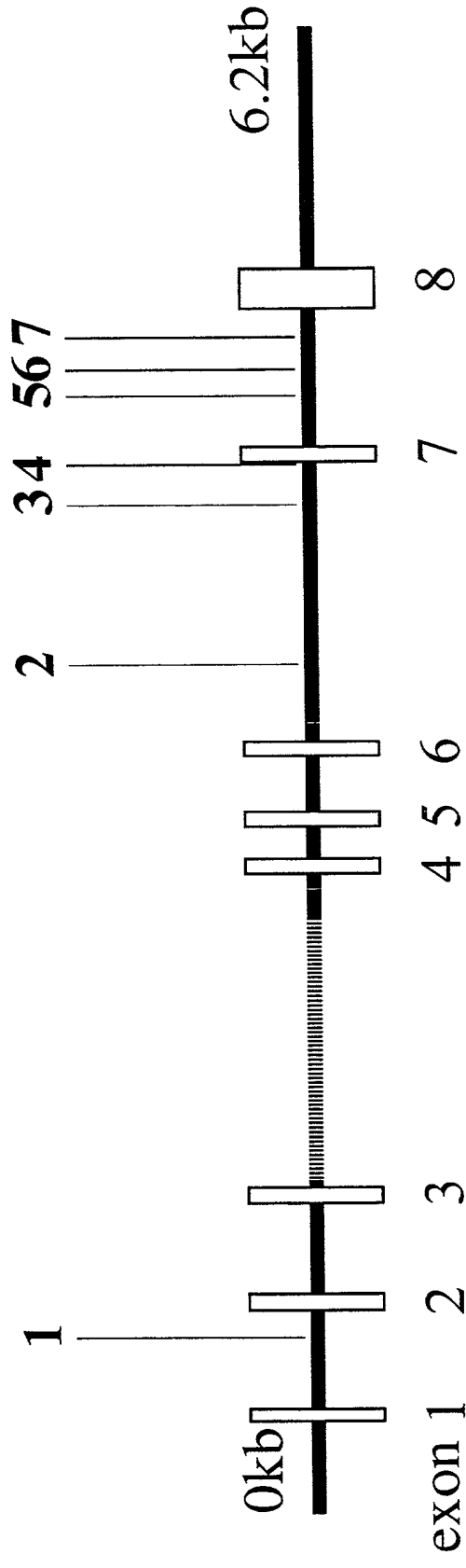


Fig. 305

*N-acetyltransferase (NAT1)*

Accession No. X17059

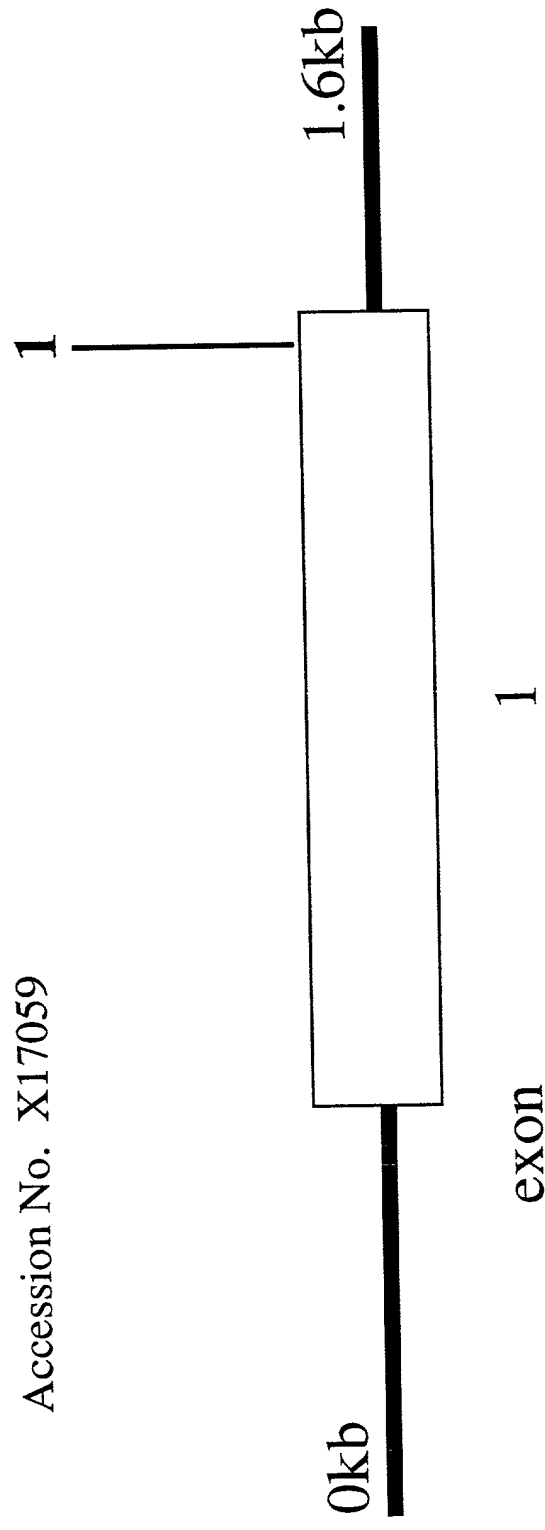




Fig. 306

*N-acetyltransferase2 (NAT2)* Accession No. D10870

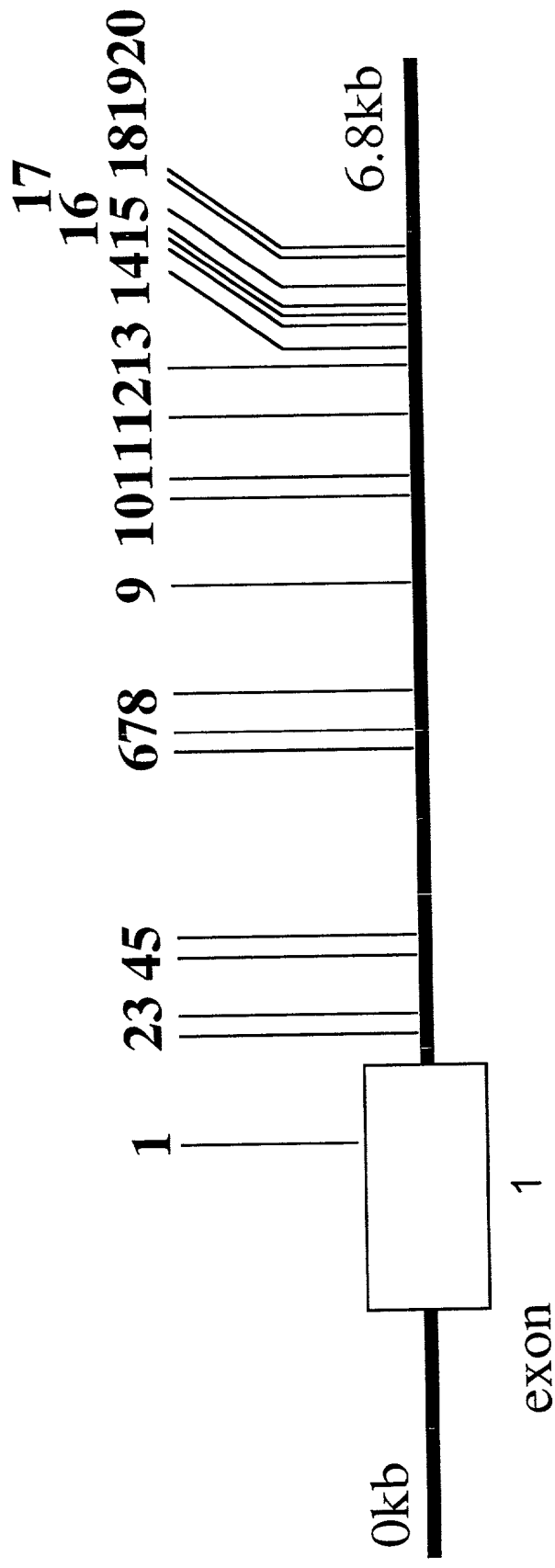


Fig. 307

ATP binding cassette, sub-family B, member 2 (ABCB2)

ACCESSION X66401

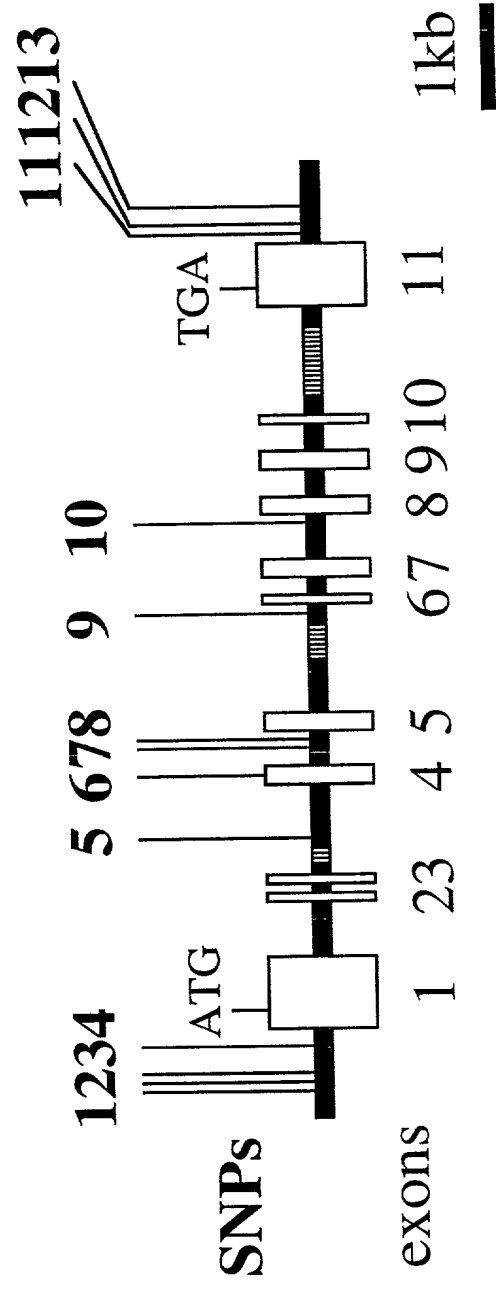


Fig. 308

ATP-binding cassette, sub-family B, member 3 (ABCB3)

ACCESSION X66401

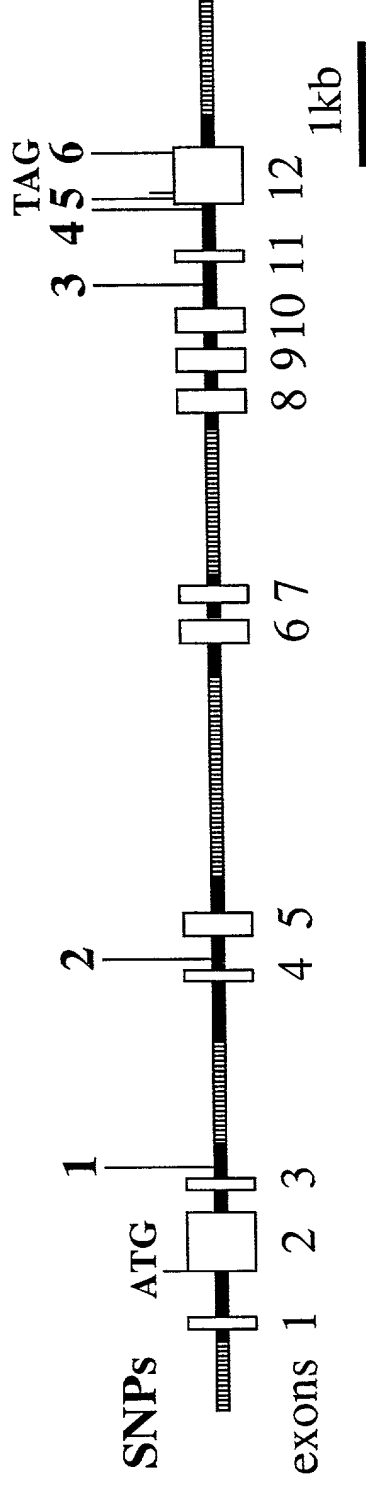


Fig. 309  
Glutathione S transferase M3 (*GSTM3*): AF043105.1

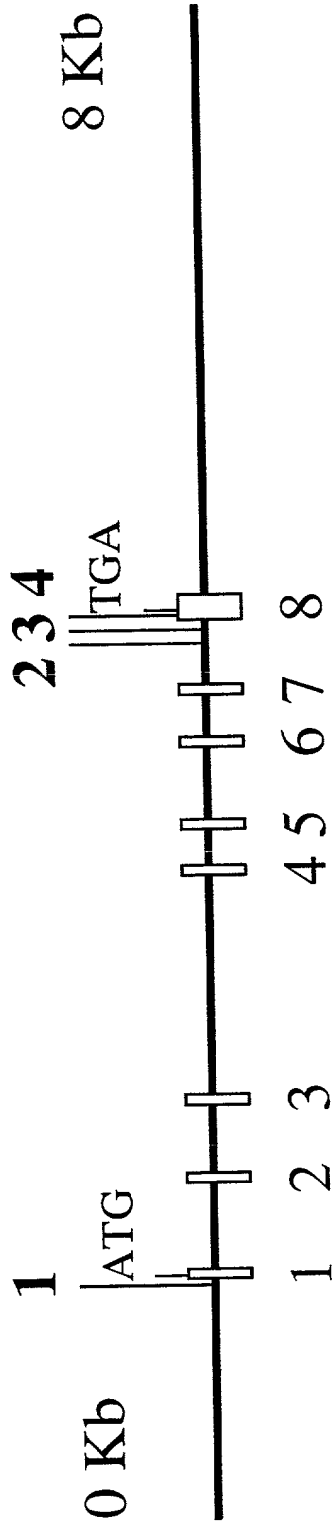


Fig. 3/D

Glutathione S transferase M4 (*GSTM4*): M96233.1

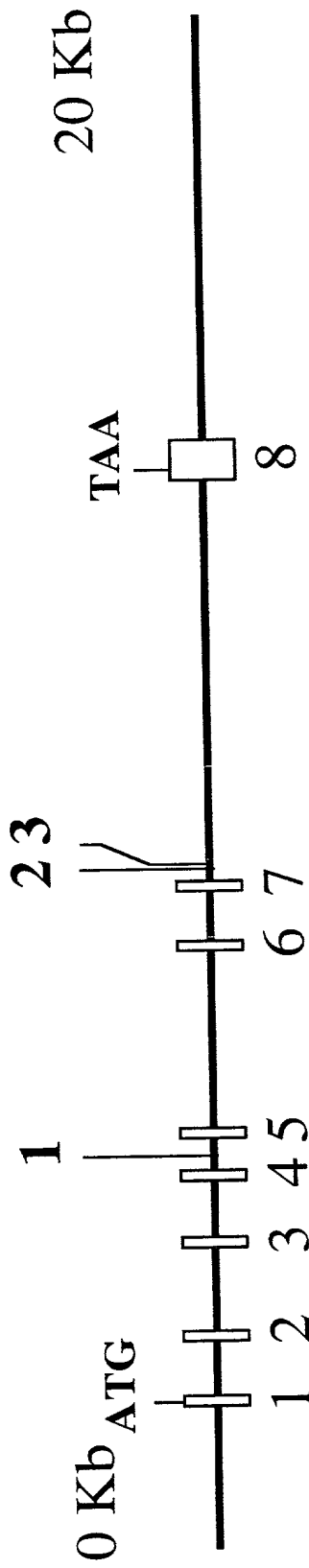


Fig. 3//

*Aldehyde dehydrogenase 7 (ALDH7)*

ACCESSION AC004923

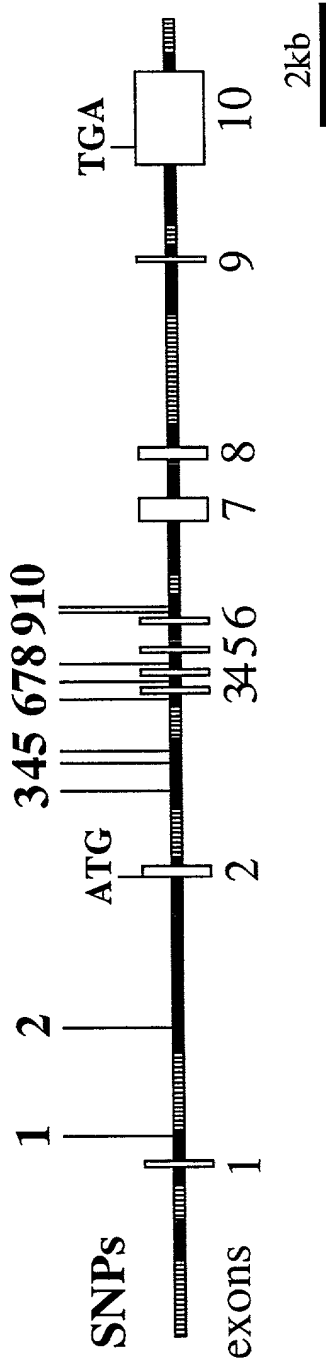
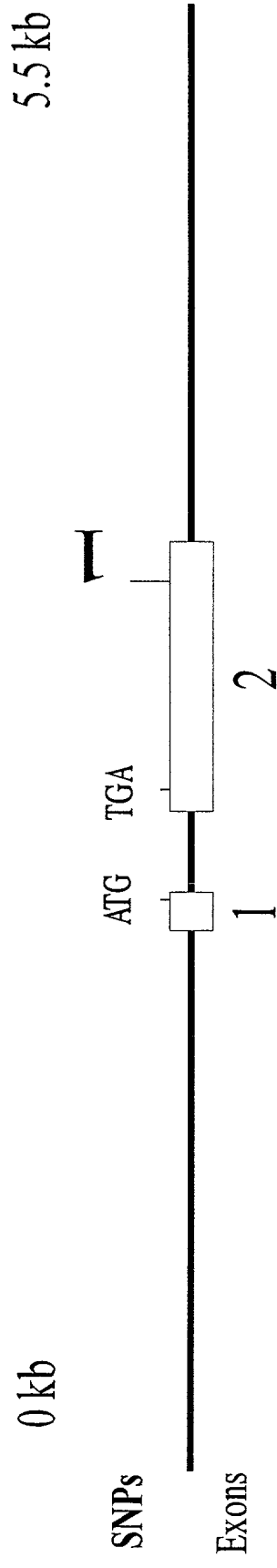


Fig. 312

High-mobility group protein 17-like 1 (*HMG17L1*)



SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

# SNP Information for IMS-JST105177

## General Information

JSNP ID : IMS-JST105177  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1184379	9	99064055

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CAGCCCCGAG CCCAGCGCTT CCCGCGCGTC TTAGCGCGGC GGGCCCGGC GGGGGAAGGG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105177](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105177)

12/17/2001



AF275948.1

Observed : G/C  
 3' Assay : ACGCAGACCG CGGACCCCTAA GACACCTGCT GTACCCCTCCA CCCCCACCCC ACCCCACCCA  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
 Chromosome :  
 map :  
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
 Position in Sequence : 1176 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_1  
 Amplified region : 276..1402 in AF275948  
 size : 1127

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TTCTACGGGT CTGTCCTGAG	
BackwardPrimer	:	AGAGTTACT ATCGGTCAA	G

663600



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105177](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105177)

## SNP Information



[SNP Home](#)

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

# SNP Information for IMS-JST105183

## General Information

JSNP ID : IMS-JST105183  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : ACCTCCTTTA AGACCCGATT TAATGCCTC CCTCCTCATG AAGCTCTTCT GGATCCACTC  
 Observed : T/C  
 3' Assay : TTCCCATCAC TAAGTTGAAA GTAAGATCCC CTTCTCTTTA CTTCCATTAG ACTTGGATTA  
 Comment :  
 Sample size : 96

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105183](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105183)

12/17/2001

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
 Chromosome :  
 map :  
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
 Position in Sequence : 7636 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : AF275948.1.20000717\_3  
 Amplified region : 7409..8565 in AF275948  
 size : 1157

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TCAGTTACTC TCCATTCTAC	G
BackwardPrimer	:	TTTGCACTCTA TACTCCAAGA	TG



## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105185

## General Information

JSNP ID : IMS-JST105185  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1196308	9	99052126

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TCCAGGCTTC TTCATACTAT ACCAGAAATT AGGATAACTA TTACAGTGCC CTTTATAGGA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105185](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105185)

12/17/2001

Observed : G/A  
3' Assay : AGAAGAAGA AATTGTGTCT GTAGATGTCT GTTCCCTTCA GCTTAAATG GACACTGAAA  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 13090 ([View SNP position in this record](#))

### Method

PCR Method  
[Sequence Method](#)

### PCR Profile

Screening region ID : AF275948.1\_20000717\_4  
Amplified region : 12939..14128 in AF275948  
size : 1190

Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCCATTACCC ACAGTGGTAG  
BackwardPrimer : AATCCACTTA CTTGTGATTC TG

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105189

## General Information

JSNP ID : IMS-JST105189  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1197894	9	99050540

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AAGTGCCCT TGCTTGATGG CATGTTTACC AGGGTTCTA GAGCCTCAAT CACAGATTCT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105189](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105189)

12/17/2001

Observed : C/G  
3' Assay : TCTAGCTCAC ATGAAGTTAA TGAAATGAA TGTGCTTCCC TACAAATTAG AGAGGCTTTG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 14676 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_5  
Amplified region : 13772..14995 in AF275948  
size : 1224

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	ATGTTAAACAC TTAGCGGTT G	
BackwardPrimer	:	GCAATGTGCA ACAAGCTACT G	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105189](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105189)

12/17/2001





12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105189](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105189)

## SNP Information



[SNP Home](#)

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

# SNP Information for IMS-JST105191

## General Information

JSNP ID : IMS-JST105191  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1203657	9	99044777

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GGAGACTTCC CTCCTCTGGA ACCTGCCCTG GCTCAGGCAT GAGGCTGAC TGTACCCCTT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105191](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105191)

12/17/2001

663600

Observed : T/C  
 3' Assay : GATAGAGCC CAGCACTAAA GCTCATGTCT TGGCAGTGT CTGCGGGA GAAAAAGAC  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
 Chromosome :  
 map :  
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
 Position in Sequence : 19522 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_6  
 Amplified region : 19125..20141 in AF275948  
 size : 1017

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGATAGAACT CTGAGAAATG C	
BackwardPrimer	:	CAATGAACTG AGAGAGTGGA C	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105191](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105191)

12/17/2001

rs112088000



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105191](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105191)

# SNP Information for IMS-JST105199

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105199  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105199](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105199)

12/17/2001

# TOGETHER

Flanking Sequence Information  
5' Assay : CTTCTCTGATT TCTAAAGGAA GTATATTTTG CTGAATCAGA AAGAAAAGTG ATTTATTTC  
Observed : A/G  
3' Assay : GTTGCTCATG CTTAGATTCT TAGAGTTGCA AAGATCTGGC TTGCAATCTTG TACAACTGAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 28790 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_11  
Amplified region : 28480..29670 in AF275948  
size : 1191  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

Forward Primer : GAATCCTGCA ACAGGATGTG

Backward Primer : ACACAAGTTA ACTGTTACTT TG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105199](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105199)

12/17/2001

## SNP Information



SNP Home

## Search

Search by HOWDY

BLAST SNP

FTP Server

### Search Example

JSNP ID	:	IMS-JST105202
dbSNP ID(rs#)	:	
dbSNP ID(ss#)	:	
HGBASE ID	:	
Organism	:	Homo sapiens
Molecular type	:	Genomic
Laboratory	:	Laboratory for
Citation	:	J Hum Genet.
Release Date	:	2001/08/09
Last Update	:	2001/08/09

**Keyword**

search

**NEW**  
**Mapping Information**

## Gene Information

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105202](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105202)

12/17/2001



# Flanking Sequence

Flanking Sequence Information  
5' Assay : CAGCCCTGCC CATTAGGTAG GGAAGAAGT TAGCAGTCCA TGATAGCTGT TGCCTGCAGC  
Observed : A/G  
3' Assay : TACGGACGTT CATTGGCAG TTCCTGTCTC CTGAGATCCT GGAGTGTATA CGCTTGGCCT  
Comment : repeat sequence (repeat sequence exists in flanking sequence)  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 29176 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_11  
Amplified region : 28480..29670 in AF275948  
size : 1191  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

# Forward Primer

ForwardPrimer : GAATCCTGCA ACAGGATGTG  
BackwardPrimer : ACACAAGTTA ACTGTTACTT TG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105202](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105202)

12/17/2001

# SNP Information for IMS-JST105205

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST105205  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105205](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105205)

12/17/2001

# Sequence

Flanking Sequence Information  
5' Assay : TAGGGGAAGA AGTTAGCAGT CCATGATAGC TGTTCCTGTC AGCATACGGA CGTTCATTGC  
Observed : G/A  
3' Assay : CAGTTCCTGT CTCTGAGAT CCTGGAGTGT ATACGCTTGG CCTCAGAGCC CAGCACAGAG  
Comment : repeat sequence (repeat sequence exists in flanking sequence)  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 29193 (View SNP position in this record)

## Method

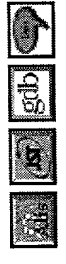
PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_11  
Amplified region : 28480..29670 in AF275948  
size : 1191  
  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

# Sequence

ForwardPrimer : GAATCCTGCA ACAGGATGTG  
BackwardPrimer : ACACAAGTTA ACTGTTACTT TG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105205](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105205)

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105206

## General Information

JSNP ID : IMS-JST105206  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1213528	9	99034906

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105206](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105206)

12/17/2001

Top of the page

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CTTGAGGAGG CTCCCTTGCA CTAGGAAGAA TAGAAGCAT ACATAAAGCC TGTGTGCTGC  
Observed : T/C  
3' Assay : GCCAGGAAGA CTAGAAACGC TATGTTTCAGC CTGGAGCTGA ATGTTATACC CCAGAGCAAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 ([Graphical View of this Entry](#))  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 29390 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1.20000717\_11  
Amplified region : 28480..29670 in AF275948  
size : 1191  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

# TOGETHER

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : GAATCCTGCA ACAGGATGTG  
BackwardPrimer : ACACAAGTGA ACTGTTACTT TG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105206](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105206)



## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105207

## General Information

JSNP ID : IMS-JST105207  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1224077	9	99024357

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105207](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105207)

12/17/2001

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTAGCACAGC AGTTGGCCT GGTCTCTCTCC TCTCAACATA GTCACCACAT ACCTGGCACT  
Observed : A/G  
3' Assay : TCCTAAGGCT GGAATGCCAG ACAGATGGGT GCCTGCTTTC AGAGTGCTCA ATGTGCTGAG  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 ([Graphical View of this Entry](#))  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 39916 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_12  
Amplified region : 39854..40990 in AF275948  
size : 1137  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

PCR "Sequence"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : ATTTAGCACA GCAGTTGGC  
BackwardPrimer : TATGCTCACT GTAAAGGCTG T



SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST105217

General Information

JSNP ID : IMS-JST105217  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1236608	9	99011826

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105217](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105217)

12/17/2001

TCCTTTCTTTCA CAAAATTGCC

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TAATAATGAT GACAGAAGTT CTTCAAAAAG TCTTGGCCTT CTTTCTTTCA CAAAATTGCC  
 Observed : C/T  
 3' Assay : CCCAGAGCTT TCTGGAAGGG CAGCCATGAA CCAGAGAGGCC TAAAGTAGAT TTAAGTGGGAA  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
 Chromosome :  
 map :  
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
 Position in Sequence : 52465 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_17  
 Amplified region : 51992..53206 in AF275948  
 size : 1215  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes  
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

# PCR "CONDITIONS"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TGTTCCTGGC TGACTGTTTG  
BackwardPrimer : ACTATGAGCC AAGTAGGACG



SNP Information



[SNP Home](#)

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105218

## General Information

JSNP ID : IMS-JST105218  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1237515	9	99010919

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105218](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105218)

12/17/2001

# PCR "PAGE"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : AGGCATACAG TGAGGGAAC  
BackwardPrimer : CAAGAGCTAC ACTGGACAC





# PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TTGTTGCTGC TCAGAAATCAT G  
BackwardPrimer : AAGGTGATAT GTCCTCCAAA G



# SNP Information for IMS-JST105219

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105219  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1243362	9	99005072

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105219](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105219)

12/17/2001

Target "CE3400"

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CCAGTCTGA CTGATTCTGG AGTGGCAGAG AGGGTTGGAG GGTACCGCT CTGCTCACCC  
Observed : G/C  
3' Assay : ACCCTCTGGC CATCTCCTCT TAGAATGCAA GGCGAGGAT TTTGTTACAC AGCGCCTCTT  
Comment :  
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 59219 (View SNP position in this record)

Method

PCR Method  
Sequence Method

PCR Profile

Screening region ID : AF275948.1\_20000717\_19  
Amplified region : 59130..60334 in AF275948  
size : 1205  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

# Test Results

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : ATGAGTAATG TCTCGTTCCA C  
BackwardPrimer : ATCACATCAG CATCCCAGGC



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105219](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105219)

SNP Information



[SNP Home](#)

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105225

## General Information

JSNP ID : IMS-JST105225  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1249738	9	98998696

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

AF275948.1

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AAGTAAACA ATGTTCTTA AACTGTGGTT CCACACCTCC CTCCTCCAAC ATTAAAAGTG  
Observed : T/C  
3' Assay : AAGGGATGCT TATTCAAATG TAGATTGTGA GGCTCTGCAC TCTAGACCCA CTATTTCAGA  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 ([Graphical View of this Entry](#))  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 65594 (View SNP position in this record)

## Method

[PCR Method](#)  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_22  
Amplified region : 65150..66351 in AF275948  
size : 1202  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

# PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : TTCACACCAG TCCTCAACTG  
 BackwardPrimer : GCCCTATGAC TCGGAAACAG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105225](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105225)

12/17/2001

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105229

## General Information

JSNP ID : IMS-JST105229  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1250219	9	98998215

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105229](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105229)



## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ACTGGCTGGG CTGTCAGGCC CTCCTGTTAC TTTATCTCTG CATGTGACCC TCTTAGCTCC  
Observed : G/A  
3' Assay : CGGATTAACT CCTGTCTCTCA TTAAGCCTCA CACTGTAGCC CCAATTTTCAG ATCAAACTCG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 66075 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1.20000717.22  
Amplified region : 65150..66351 in AF275948  
size : 1202  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TTCACACCAG TCCTCAACTG  
BackwardPrimer : GCCCTATGAC TCCGAAACAG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105229](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105229)

# SNP Information for IMS-JST105238

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105238  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1255690	9	98992744

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105238](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105238)

12/17/2001

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : ATTGTGGGCT GTACAGTTG GAAGGCCCTG GAATTAGATG AGACCACT ACTTAGCTTA  
 Observed : C/T  
 3' Assay : TTAGTAATAA CATTGCAAG AAAAATTCG ACGAAGTTT TTCAGCCTAG GAATCAATAG  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
 Chromosome :  
 map :  
 Definition of the record : Homo sapiens ABCAL (ABCA1) gene, complete cds.  
 Position in Sequence : 71478 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_25  
 Amplified region : 70681..71942 in AF275948  
 size : 1262  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes  
 Annealing : 60.0 degrees C for 0.50 minutes

Test "E3E00"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : AGACCTGATG CATTGGACTG  
BackwardPrimer : AAGTCACAT TCTAGGGTAT G



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105238](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105238)

PCR Cycle

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TGTCAGGAAG CAGCAGTGAT	
BackwardPrimer	:	ACATTTCAG ATATCAGCTA C	



TCCTGATGTTGGTTTATGACCAAGGTATGATTAAAGGTGGCTACTACC

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TGGTTGTGCC TTGTGGATGC GTTGGTTTAT GACCAAGGTAT GATTAAAGGT GGCTACTACC  
Observed : A/G  
3' Assay : GGTGCTTTCT GCATATCTCG GGTGTGTGGA GCACTCAGGT TCTGCTTCTG CCCCTCTGCT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 73129 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_26  
Amplified region : 72579..73742 in AF275948  
size : 1164  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

# PCR condition

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : AGTTAGAGAA GCTGACTTGT G  
BackwardPrimer : ACTGCCATAC TTCCCATG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105242](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105242)

12/17/2001



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105261

## General Information

JSNP ID : IMS-JST105261  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1275854	9	98972580

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105261](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105261)

12/17/2001

TCAGCT#GGGGGGT

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TGAACAACAT GGAGGCTG GCATGAGAGT GTGAATCTGG ATGGGAGGGC TTGTGCTTCA  
Observed : T/C  
3' Assay : GAAACATTT TTCCAGATCA GCTCAGTCGT GAGTTATCCG TCATTGACGT TATAATAAGC  
Comment : repeat sequence (repeat sequence exists in flanking sequence)  
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 91642 (View SNP position in this record)

Method

PCR Method  
Sequence Method

PCR Profile

Screening region ID : AF275948.1.20000717.35  
Amplified region : 91500..92700 in AF275948  
size : 1201  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075566

## General Information

JSNP ID : IMS-JST075566  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403406	4	68103408

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TCACCTTTGC CTCATACAGG TAAATCTAAG AAAGTAGGGA CTATGAGAAC CCCATATGTAT

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075566](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075566)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST105263  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1276632	9	98971802

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105263](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105263)

12/17/2001

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GGAGGAGCCA AACGCTCATT GTCTGTGCTT CTCTCCTTT TTCTGCGGTC CCTGGCTCCC  
Observed : C/T  
3' Assay : ACCTGACTCC AGGTGAACAA GACCTTCCAG GAACTGGCTG TGTCCAAGA TCTGGAAGGC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 92420 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_35  
Amplified region : 91500..92700 in AF275948  
size : 1201  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

# TOGETHER

Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : TTGCTTGAAA ACTGAGGTCT G  
 BackwardPrimer : GTGGTGCCCT GTGACTTTAG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105263](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105263)

12/17/2001

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST105269

General Information

JSNP ID : IMS-JST105269  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1281507	9	98966927

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Top of the page

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TATCTCAGTG ACTAATGGTA GCAAAGCATT CCCTTAAAAA GGCATTATTT GTGAAACTTA  
Observed : T/C  
3' Assay : CTAAATCGA ATTCCGGTCC AATTAAATTT TTGAAATTTT ATATTAAAAA TTATATTAGT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 97295 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_38  
Amplified region : 96698..97787 in AF275948  
size : 1090  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001



# PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : GTAGTGCTCC TCAAGATTTA G  
BackwardPrimer : AACTTCCTCT CATCCAGCAG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105273

## General Information

JSNP ID : IMS-JST105273  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1286207	9	98962227

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105273](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105273)

12/17/2001

# Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ATCAAGAGGG AAGTCAAGT TGCCTGGCCA TTTTCCTTGG CTTTAGACA GAAAAGTTAC  
Observed : G/A  
3' Assay : TGGGATATTA TCTCCACAG CTCCTCTGTG GTGCCACCAG TCATAGTCCT TATATAAGGA  
Comment :  
Sample size : 96

# Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCAL (ABCAL) gene, complete cds.  
Position in Sequence : 101995 (View SNP position in this record)

# Method

PCR Method  
Sequence Method

# PCR Profile

Screening region ID : AF275948.1\_20000717\_40  
Amplified region : 101849..102994 in AF275948  
size : 1146  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

## PCR "SEQUENCE"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CCTGCAGACA TGTACCCATC  
BackwardPrimer : CAAGAGAGGT CATCTCTGAC



**SNP Information for IMS-JST105285**



SNP Home

## Search

TSNP ID : IMS-JST105285

dbSNP ID(rs#)

dbSNP ID(rs#)

Search by HOWDY

dbSNP ID (ss#)

HGBASE ID

HGBASE ID

BLAST SNP

Homo sapiens

Molecular type

## Genomic

## FTP Server

Laboratory

Laboratory for Genotyping, The SNP Research Center, RIKEN

Citation

J Hum Genet. (in press)

### Search Example

Release Date

2001/08/09

Last Update

2001/08/09

**Keyword**

\_\_\_\_\_

search

## NEW Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1293242	9	98955192

## Gene Information

## Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105285](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105285)

12/17/2001

Variation Type	:	SNP	
Flanking Sequence	:	Information	
5', Assay	:	TTTCTCTTA	TCTAAAGTGA
Observed	:	C/T	ACAGCTGGG
3', Assay	:	ACATGGGGCT	CATGTGCAG
Comment	:		GTCTCCCG
Sample size	:	96	CTGAGTCC
	:		CTGAGGCTCA

Accession No.	:	AF275948.1	(Graphical View of this Entry)
Chromosome	:		
map	:		
Definition of the record	:	Homo sapiens ABCA1 (ABCA1) gene, complete cds.	
Position in Sequence	:	109030 (View SNP position in this record)	

PCR Method  
Sequence Method

```

Screening region ID : AF275948.1_20000717_44
Amplified region   : 108579..109721 in AF275948
size                : 1143

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes
Annealing          : 60.0 degrees C for 0.50 minutes

```

Variable	Mean	SD	Range
Age	34.5	7.2	20-55
Gender	50%	50%	Male/Female
Marital status	65%	35%	Married/Single
Education	12.5	1.5	10-16
Occupation	1.5	1.0	1-5
Income	1.5	1.0	1-5
Health status	1.5	1.0	1-5
Stress level	1.5	1.0	1-5
Life satisfaction	1.5	1.0	1-5
Work satisfaction	1.5	1.0	1-5
Family satisfaction	1.5	1.0	1-5
Healthcare satisfaction	1.5	1.0	1-5
Overall satisfaction	1.5	1.0	1-5
Healthcare access	1.5	1.0	1-5
Healthcare quality	1.5	1.0	1-5
Healthcare cost	1.5	1.0	1-5
Healthcare convenience	1.5	1.0	1-5
Healthcare safety	1.5	1.0	1-5
Healthcare effectiveness	1.5	1.0	1-5
Healthcare equity	1.5	1.0	1-5
Healthcare transparency	1.5	1.0	1-5
Healthcare accountability	1.5	1.0	1-5
Healthcare responsiveness	1.5	1.0	1-5
Healthcare communication	1.5	1.0	1-5
Healthcare education	1.5	1.0	1-5
Healthcare research	1.5	1.0	1-5
Healthcare innovation	1.5	1.0	1-5
Healthcare leadership	1.5	1.0	1-5
Healthcare governance	1.5	1.0	1-5
Healthcare regulation	1.5	1.0	1-5
Healthcare policy	1.5	1.0	1-5
Healthcare strategy	1.5	1.0	1-5
Healthcare vision	1.5	1.0	1-5
Healthcare mission	1.5	1.0	1-5
Healthcare values	1.5	1.0	1-5
Healthcare culture	1.5	1.0	1-5
Healthcare climate	1.5	1.0	1-5
Healthcare environment	1.5	1.0	1-5
Healthcare community	1.5	1.0	1-5
Healthcare network	1.5	1.0	1-5
Healthcare system	1.5	1.0	1-5
Healthcare organization	1.5	1.0	1-5
Healthcare management	1.5	1.0	1-5
Healthcare administration	1.5	1.0	1-5
Healthcare operations	1.5	1.0	1-5
Healthcare services	1.5	1.0	1-5
Healthcare products	1.5	1.0	1-5
Healthcare technology	1.5	1.0	1-5
Healthcare innovation	1.5	1.0	1-5
Healthcare research	1.5	1.0	1-5
Healthcare development	1.5	1.0	1-5
Healthcare implementation	1.5	1.0	1-5
Healthcare evaluation	1.5	1.0	1-5
Healthcare monitoring	1.5	1.0	1-5
Healthcare assessment	1.5	1.0	1-5
Healthcare analysis	1.5	1.0	1-5
Healthcare synthesis	1.5	1.0	1-5
Healthcare conclusion	1.5	1.0	1-5
Healthcare recommendation	1.5	1.0	1-5
Healthcare suggestion	1.5	1.0	1-5
Healthcare advice	1.5	1.0	1-5
Healthcare guidance	1.5	1.0	1-5
Healthcare instruction	1.5	1.0	1-5
Healthcare direction	1.5	1.0	1-5
Healthcare supervision	1.5	1.0	1-5
Healthcare oversight	1.5	1.0	1-5
Healthcare management	1.5	1.0	1-5
Healthcare administration	1.5	1.0	1-5
Healthcare operations	1.5	1.0	1-5
Healthcare services	1.5	1.0	1-5
Healthcare products	1.5	1.0	1-5
Healthcare technology	1.5	1.0	1-5
Healthcare innovation	1.5	1.0	1-5
Healthcare research	1.5	1.0	1-5
Healthcare development	1.5	1.0	1-5
Healthcare implementation	1.5	1.0	1-5
Healthcare evaluation	1.5	1.0	1-5
Healthcare monitoring	1.5	1.0	1-5
Healthcare assessment	1.5	1.0	1-5
Healthcare analysis	1.5	1.0	1-5
Healthcare synthesis	1.5	1.0	1-5
Healthcare conclusion	1.5	1.0	1-5
Healthcare recommendation	1.5	1.0	1-5
Healthcare suggestion	1.5	1.0	1-5
Healthcare advice	1.5	1.0	1-5
Healthcare guidance	1.5	1.0	1-5
Healthcare instruction	1.5	1.0	1-5
Healthcare direction	1.5	1.0	1-5
Healthcare supervision	1.5	1.0	1-5
Healthcare oversight	1.5	1.0	1-5
Healthcare management	1.5	1.0	1-5
Healthcare administration	1.5	1.0	1-5
Healthcare operations	1.5	1.0	1-5
Healthcare services	1.5	1.0	1-5
Healthcare products			

Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTTTGAATAT	GGCAGGCTCA C
BackwardPrimer	:	CAAGTTTCTG	TTACCAACGG C



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105285](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105285)

12/17/2001

# SNP Information for IMS-JST105289

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST105289  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1295180	9	98953254

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105289](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105289)



## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CAGCCAGGAC TTGCTGGCTG TGAATGATTT CTCCATCTCC ACCCCTTTTG CCAIGTTGAA  
Observed : A/G  
3' Assay : CCACCATCTC CCTGCTCTGT TGCCCCCTTG AAATCATATC ATACTTAAGG CATGGAAGC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 110968 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_46  
Amplified region : 110159..111199 in AF275948  
size : 1041  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

PCR "E3E00"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : GGTTAGTTGA AAGGTGGAT G  
BackwardPrimer : ATGAGCAGGA ACACCAGGTC



# SNP Information for IMS-JST105294

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105294  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1299776	9	98948658

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105294](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105294)

12/17/2001

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AAGTGCATAG ATCCCTACAG AGTCCAAGA GAAGTGAGGA AATGGTAAAA GCCACTTGT  
Observed : C/T  
3' Assay : TTTGCAGCAT CGTGCATGTG ATCAAACCTG AAAGAGCCTA TCCATATCAC TTCCTTTAAA  
Comment :  
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 115563 (View SNP position in this record)

Method

PCR Method  
Sequence Method

PCR Profile

Screening region ID : AF275948.1\_20000717\_49  
Amplified region : 114846..115694 in AF275948  
size : 849  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

--- SNP INFORMATION ---

PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TGATAGCTCT CACCACTGAG  
BackwardPrimer : AAGAAACTAG GACCCCGCAG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105294](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105294)

12/17/2001

FB2222T 2222222

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

# SNP Information for IMS-JST105296

## General Information

JSNP ID : IMS-JST105296  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1302524	9	98945910

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GCCCAATGTA GTCTTTCTCA GTCTTCAGGA GGAGGAAGGG CAGGACCCAG TGTTCAGT  
Observed : C/T  
3' Assay : ACCCTGAATG TGAGCACTAT TTACTTCGTG AACTTCTTGG CTTAGTGCCT CTGCCAGGTG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 118311 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_50  
Amplified region : 117331..118503 in AF275948  
size : 1173  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

# TOGETHER

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TCAGCTGTCA TAACATGAGA G  
BackwardPrimer : GACCAACCAG CACGGCAATG





# SNP Information for IMS-JST105297

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105297  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1304647	9	98943787

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105297](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105297)

12/17/2001

TOP SECRET

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CCCAGCCCCT GTACTTAAGT GCTTCAATAG GCTCTCATTA TATATGATTT TTAGGTTTTG  
 Observed : T/C  
 3' Assay : TTATCAGCCTT CTTCGCTTTT ATAATCTGAA AAGATGGCAT ATGAATTTTT ATAAAAAGGG  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
 Chromosome :  
 map :  
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
 Position in Sequence : 120434 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_51  
 Amplified region : 120141..121315 in AF275948  
 size : 1175  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes  
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

# PCR "EFFECT"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TGCATGCCAC ATTGTGACCG  
BackwardPrimer : GGGCTCAGAC ATCATGTTTG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105297](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105297)

# SNP Information for IMS-JST105299

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

## General Information

JSNP ID : IMS-JST105299  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HCBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1305308	9	98943126

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP\\_ID=IMS-JST105299](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-JST105299)

12/17/2001

### Allele Sequence

Variation Type : SNP  
Flanking Sequence : Information  
5' Assay : CCAGATGACA AGGATAGAGA AGGACACAGA CACGGCCTAT CTGGATTCA TGGTGCCITTT  
Observed : G/C  
3' Assay : ATTTCCACA TGAAGTTGT GTAGGGAAGA TAGAAGCATG AGATGAGATG ATAATATAGT  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

### Screened Sequence

Accession No. : AF275948.1 ([Graphical View of this Entry](#))  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 121095 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : AF275948.1\_20000717\_51  
Amplified region : 120141..121315 in AF275948  
size : 1175  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

# PCR "E3E00"

Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : TGCATGCCAC ATTGTGACCG  
 BackwardPrimer : GGGCTCAGAC ATCATGTTTG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105299](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105299)

# SNP Information for IMS-JST105301

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105301  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1311083	9	98937351

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105301](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105301)

## Allele Sequence

Variation Type	:	SNP
Flanking Sequence	:	Information
5' Assay	:	AAAATGAGAT AGGTGATGTG GCTACGTCAG GGGGCCCGAA GGCTCCTTGT TACTGATTTC
Observed	:	C/T
3' Assay	:	GTCCTTTTTC TCTGCCTTTT CCCCAAGGC CAGGACCCCT GGATCTCTGG GCAGAGCAGA
Comment	:	
Sample size	:	96

## Screened Sequence

Accession No.	:	AF275948.1	(Graphical View of this Entry)
Chromosome	:		
map	:		
Definition of the record	:	Homo sapiens ABCA1 (ABCA1) gene, complete cds.	
Position in Sequence	:	126866	(View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

```

Screening region ID : AF275948.1_20000717_53
Amplified region   : 126539..127601 in AF275948
size               : 1063

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes
Annealing          : 60.0 degrees C for 0.50 minutes

```



# PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : TGCAGGTGTC TAGGGATTTC  
 BackwardPrimer : CCAAAGACGG CTCTGTATGC





TGAGGT "GGGGGT"

## Allele Sequence

Variation Type : SNP  
Flanking Sequence : Information  
5' Assay : CCACTGGGTT GGAGGAGCAT CTGTGAGATG AAACACCAATT CTTTCCTCAA TGTCACAGCT  
Observed : A/G  
3' Assay : TCTAACTGTG TGTGTAATCA GGCCAGGTCC TCCTGTGCTGG GCAGAAACCA TGGGAGTTAA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 127129 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_53  
Amplified region : 126539..127601 in AF275948  
size : 1063  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

0434T" 663600T

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TGCAGGTGTC TAGGGATTTC  
BackwardPrimer : CCAAGACGG CTCTGTATGC



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105304](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105304)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST105312  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1319606	9	98928828

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	



--- SNP INFORMATION ---

Test "E686001"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : ATACTCAG CATTCTCCA G  
BackwardPrimer : AGCCCTCTT CTATGAACAG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105312](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105312)

# SNP Information for IMS-JST105319

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105319  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1321488	9	98926946

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105319](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105319)

12/17/2001



TTATTTTCTTTT

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTAATTTTAA AAATACCTGC AATACATATA TATCTTGAAT AGATGAAAAA TTATGTAGAT  
Observed : G/A  
3' Assay : ATAATGAATG ATACGTTCT AAAAAAGACAG GTTAAAAAGT AAGTTCACCTT TTATTTTGAG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
Map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 136783 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : AF275948.1.20000717\_61  
Amplified region : 136633..137272 in AF275948  
size : 640  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CCTCTAGATG CCAGCATCTC  
BackwardPrimer : ATTCTCTTGA CATACAGGT C



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105319](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105319)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST105320

General Information

JSNP ID : IMS-JST105320  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1321501	9	98926933

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TACCTGCAAT ACATATATAT GTTGAATAGA TCAAAAATTA TCTAGATGAT AATGAATGAT  
Observed : A/G  
3' Assay : CGGTTCTAAA AAGACAGGTT AAAAAGTAAG TTCACCTTTTA TTTTGAGCTT CAGAAATCATT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 136796 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : AF275948.1\_20000717\_61  
Amplified region : 136633..137272 in AF275948  
Size : 640  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

# PCR "SCREEN"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CCTCTAGATG CCAGCATCTC  
BackwardPrimer : ATTCTCTTGA CATACAGGT C



# SNP Information for IMS-JST105324

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105324  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1323098	9	98925336

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105324](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105324)

12/17/2001

Table 1	
Summary of the study	
Study design	Retrospective cohort study
Study period	1990-1999
Study location	United States
Study population	Adults aged 18 years and older
Study variables	Age, sex, race, education, income, health status, and health behaviors
Study results	Health status and health behaviors are associated with health outcomes
Study limitations	Retrospective design, self-reported data, and potential confounding
Study conclusions	Health status and health behaviors are important determinants of health outcomes

## Screened Sequence

## Method

# PCR Profile

```

Screening region ID : AF275948.1_20000717_62
Amplified region   : 137780..13813 in AF275948
size               : 1034

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes
Annealing          : 60.0 degrees C for 0.50 minutes

```

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105324](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105324)

Test "66666666"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CTTGGCCTC AACTGACAA C  
BackwardPrimer : AAATGGCCTA ACGGTGGCTC





SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

# SNP Information for IMS-JST105327

## General Information

JSNP ID : IMS-JST105327  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. (in press)  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1324484	9	98923950

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GCAGTAATAA CCAGCCCATTA GTAAGTTTG TCACAGGGAC TGGTTGTAAG AACTGATTTG  
Observed : G/A  
3' Assay : TTGGTATAGC TGTGAGGGCC TGGCACGGTG TCCACGTGTG CCTCAATCCT AATTCTGAAA  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : AF275948.1 ([Graphical View of this Entry](#))  
Chromosome :  
map :  
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.  
Position in Sequence : 139779 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : AF275948.1\_20000717\_63  
Amplified region : 138622..139911 in AF275948  
size : 1290  
  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes

Protocol "E63E007"

Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CCCCTATGT ACATGTACCT  
BackwardPrimer : GCCATGAAC TGGCCTTCTG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105335

## General Information

JSNP ID : IMS-JST105335  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HCBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1331322	9	98917112

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TTGTTTGGG AAGTTCAAGT GATCTTCAA TATCATTAAT AACTTCTTCC ACTTTTCCA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105335](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105335)

12/17/2001

[illegible]

Accession No.	:	AF275948.1 (Graphical View of this Entry)
Chromosome	:	
map	:	
Definition of the record	:	Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence	:	146617 (View SNP position in this record)

## PCR Profile

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105335](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105335)

Font: "E6E9E907"



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105335](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105335)

12/17/2001

TSST 6636007

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## SNP Information for IMS-JST105336

### General Information

JSNP ID : IMS-JST105336  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. (in press)  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

### Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1331337	9	98917097

### Gene Information

### Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CAAGTGATCT TTCAATATCA TTACTAACTT CTTCACCTTT TTCAGAAAT TGAATATTAA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105336](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105336)

12/17/2001

```
Observed      : C/T
3' Assay      : GCT
Comment       :
Sample size    : 96
```

## Screened Sequence

```

Accession No.      : AF275948.1 (Graphical View of this Entry)
Chromosome         :
map               :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence   : 146632 (View SNP position in this record)

```

## Method

[illegible]

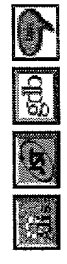
## PCR Profile

Screening region ID	:	AF275948.1_20000717_68			
Amplified region	:	146071..14732 in AF275948			
size	:	1162			
Pre-Denature	:	94.0 degrees	C for	2.00 minutes	
Denaturation	:	94.0 degrees	C for	0.50 minutes	
Annealing	:	60.0 degrees	C for	0.50 minutes	
Polymerization	:	72.0 degrees	C for	2.00 minutes	
PCR Cycles	:	35			
Post-Extension	:	72.0 degrees	C for	7.00 minutes	
ForwardPrimer	:	GTCTCAGTAC	ACTTCTCTGTG		
BackwardPrimer	:	CATAGTACA	TTCACAGGG	A	

12/17/2001



# TOGETHER



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105336](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105336)

12/17/2001

# SNP Information for IMS-JST105354

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105354  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022863.5	505008	4	97016801

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022863.3	genomic	ADH3	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105354](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105354)

12/17/2001

Top of Page

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TCGAGAAGGG GTGACTACAG TCACACCAGG TACAGGATTC AACTCAGGG AACATGCCTT  
 Observed : G/A  
 3' Assay : GTTCACCATC ACAAGATTAG TCAGCCTGGA TGAGGAACC GAGGCAATGA AAGACGAAAG  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_022863.3 ([Graphical View of this Entry](#))  
 Chromosome : 4  
 map  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
 Position in Sequence : 876996 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_022863.3.20010416.11  
 Amplified region size : 876463..877418 in NT\_022863 : 956  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105354](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105354)

12/17/2001

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : GCAAGGGAT ATATATCAAG AG  
 BackwardPrimer : TTCTTCAGCC GTAACCATGC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

# SNP Information for IMS-JST105373

## General Information

JSNP ID : IMS-JST105373  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022863.5	592850	4	96928959

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022863.3	genomic	ADH7	intron*1	Annotated	

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CCAGGAAGCC AAATGTTTCC ACAAGGACAC TTCAATCGTC TCAGTAGCAT GTGCTGCAC  
Observed : C/T  
3' Assay : GCTGCAGTAG TTCAATGGGA AACCAGGGTC TCATGCCCAG ATGTTGGAAG AAACGTTCC  
Comment :  
Sample size : 96

Screened Sequence

Accession No. : NT\_022863.3 (Graphical View of this Entry)  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 789151 (View SNP position in this record)

Method

PCR Method  
Sequence Method

PCR Profile

Screening region ID : NT\_022863.3\_20010416\_20  
Amplified region : 788920..790047 in NT\_022863  
size : 1128  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "EFFECT"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : AGGCATACAG TGAGGGAAC  
BackwardPrimer : CAAGAGCTAC ACTGGACAC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105382

## General Information

JSNP ID : IMS-JST105382  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022863.5	572822	4	96948987

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022863.3	genomic	ADH7	intron*1	Annotated	



TCATGCTATTT ATTCAAGTA

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CTAGTTGATT TCATTGGGC TATTTTATT TCATCATAAA GCTGCTATTT ATTCAAGTA  
Observed : G/A  
3' Assay : GCCACAAAAT TTCCTTATTT TACAGTTTTC AAAGTGCTTT CTCAAATGNG CATTATTCAG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_022863.3 (Graphical View of this Entry)  
Chromosome : 4  
map :  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 809180 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_022863.3.20010416.25  
Amplified region : 808358..809409 in NT\_022863  
size : 1052  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TGTCTAAGA GAAATGTGT GC  
BackwardPrimer : GCTTGCCAAG CTCTGTCAGA



TOP "663600"

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

# SNP Information for IMS-JST075392

## General Information

JSNP ID : IMS-JST075392  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	333322	22	40631461

## Gene Information

Locus Link ID : 25830  
 Gene Name : sulfortranferase family 4A, member 1  
 Gene symbol : SULT4A1  
 Alias symbol : SULTX3, BR-STL-1, DJ388M5.3  
 Product : sulfortranferase family 4A, member 1

## Relation to gene sources

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\_ID=IMS-JST075392

12/17/2001

NT 011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology
				25830

View predicted exons with Unigene : Hs.189810

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GGCCAGACTG TCCCCCGTGT GTGCAGATTG ACTAGATCCC TGCTTCGGGC TGGGCTTGGC  
 Observed : G/A  
 3' Assay : GGGGCAGCTG TGCTCCAGGC ACCTCTTTT CTCTTCTGG GACTAGCAGC CTAGCCTGGG  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT 011521.1 ([Graphical View of this Entry](#))  
 Chromosome : 22  
 map :  
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
 Position in Sequence : 333322 ([View SNP position in this record](#))

## Method

PCR Method  
 Sequence Method

NT\_011521.1\_20010416\_5

# PCR Profile

Screening region ID : NT\_011521.1\_20010416\_5  
Amplified region size : 332741..333825 in NT\_011521  
size : 1085

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGCTTTTCGT ACTAGAGAGT G	
BackwardPrimer	:	ACCTTCAGAC AGAGCTGGCA	



CTCTGACAG CGAAGATCAG

BackwardPrimer : CTCTGACAG CGAAGATCAG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075522](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075522)

12/17/2001

# Footnote

NT_011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology 25830

view predicted exons with Unigene : [Hs.189810](#)

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TCTGATGCTT TCTGTGAGTT CTGGTGGGAA TTTTGATGGG CTCTGTGCCC GGTGTTGAGA  
Observed : C/A  
3' Assay : AGGCCATGCC CTAGAGTCCT GGRGAGTTCC ACCCCAGAAC AGCAGTGGCC TCCCACAGGC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : [NT\\_011521.1](#) ([Graphical View of this Entry](#))  
Chromosome : 22  
map :  
Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
Position in Sequence : 328070 ([View SNP position in this record](#))

## Method

[PCR Method](#)  
[Sequence Method](#)

NT\_011521.1\_20010416\_10

## PCR Profile

Screening region ID : NT\_011521.1\_20010416\_10  
Amplified region : 327311..328210 in NT\_011521  
size : 900

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GCAACTGGTG AATCCTGTGA	
BackwardPrimer	:	ACACGCCACA GTCTCACAGC	





SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075406

## General Information

JSNP ID : IMS-JST075406  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	319066	22	40617205

## Gene Information

Locus Link ID : 25830  
Gene Name : sulfortranferase family 4A, member 1  
Gene symbol : SULT4A1  
Alias symbol : SULTX3,BR-STL-1,DJ388M5.3  
Product : sulfortranferase family 4A, member 1

## Relation to gene sources

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075406](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075406)

12/17/2001

NT_011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology
				25830

View predicted exons with Unigene : Hs.189810

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TGACCCCTCC GCTACCCCTAG ACCGCCCGTT CCCTCTGATA ACTCCACTTC CCCTGAACCC  
Observed : C/T  
3' Assay : ACCCCTTCCT TCCTCCTCTG GCCCCTTCC CTTGGCCCC ACTCCTCCCC TTGGTCTCAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_011521.1 ([Graphical View of this Entry](#))  
Chromosome : 22  
map :  
Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
Position in Sequence : 319066 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

NT\_011521.1\_20010416\_12

PCR Profile

Screening region ID : NT\_011521.1\_20010416\_12  
Amplified region size : 318563..319331 in NT\_011521  
size : 769

Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CCGAGACTCT CTCCAGGACA  
BackwardPrimer : CAGGCCTTGG CATTGATGC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075407

## General Information

JSNP ID : IMS-JST075407  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	312854	22	40610993

## Gene Information

Locus Link ID : 25830  
Gene Name : sulfortranferase family 4A, member 1  
Gene symbol : SULT4A1  
Alias symbol : SULTX3,BR-STL-1,DJ388M5.3  
Product : sulfortranferase family 4A, member 1

## Relation to gene sources

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075407](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075407)

12/17/2001

0431 " CCGGGG

NT_011521.1	genomic	SUL/T4A1	intron*1	Annotated	
Hs.189810	mRNA	SUL/T4A1	intron*3	Homology	25830

view predicted exons with Unigene : Hs.189810

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CCTTCTCAGA GGCTGTCACC CCCATGGTCA GGCTTCAAG GCCTGCCGAA GCGGGGAGGG  
 Observed : C/T  
 3' Assay : TGGGATGGCT CAAGACGTGA GTGCCTCGGG GGCCTTTGCC AGACTTGTC GCAGGGGATCA  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011521.1 ([Graphical View of this Entry](#))  
 Chromosome : 22  
 map :  
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
 Position in Sequence : 312854 ([View SNP position in this record](#))

## Method

PCR Method  
 Sequence Method

NT\_011521.1\_20010416\_13

PCR Profile

Screening region ID : NT\_011521.1\_20010416\_13  
Amplified region size : 478

Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 54.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CACTTGTTAA GCGATAAAG T  
BackwardPrimer : ACTGTAAAGG GCTCCTGGGT



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075407](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075407)

12/17/2001

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075445

## General Information

JSNP ID : IMS-JST075445  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027064.2	268465	7	64313288

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TTTAAGGAAG GCAGCAGGAA AATAGAACAA GTGAATATTT TAYGTTCTTA GTGGTTTATG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075445](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075445)

12/17/2001

# PCR REACTION

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : AGGTGGATGG GTGGATGACT  
BackwardPrimer : GAAGACGAAG TGAGAGGCTG CT





[illegible]

BackwardPrimer : ACGTATTCAG ATCCCAAATT CA



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075445](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075445)

12/17/2001

# SNP Information for IMS-JST075449

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST075449  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027064.2	523034	7	64567857

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CAGCCACAAG TCCCTGGAC CTCAGAGAAT GTATATACTG TATGTGCACC CTAATAACAT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075449](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075449)

12/17/2001

10038833 400701

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075449

General Information

JSNP ID : IMS-JST075449  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027064.2	523034	7	64567857

Gene Information

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CAGCCACAAG TCCCTGGAC CTCAGAGAAT GTATATACTG TATGTGCACC CTAATAACAT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075449](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075449)

12/17/2001

# Footnote

Observed : A/G  
3' Assay : TTTCCTTAA ACTAGTACTA CTGGATCCTC TAACTTTAGT ACATGTCTTT CATGTCCAAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_007720.3 (Graphical View of this Entry)  
Chromosome : 7  
map  
Definition of the record : Homo sapiens chromosome 7 working draft sequence  
e segment.  
Position in Sequence : 411047 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_007720.3.20010416\_6  
Amplified region : 410221..411418 in NT\_007720  
size : 1198

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AAAGCTAAGA GTGGCCTGAG	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075465  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6176321	22	23428109

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

TCCTCTGTTGC

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GCTCTGTTGC CCAAGCTGGG TGCACCTGGTG CAGTCATAGC TACTGCAGCC TGATACTTCI  
 Observed : C/T  
 3' Assay : GGCTTAAGCC ATCCTCTCAC CCCAGGCTCC TGAGTAGYTA GGA CTGCAGG TGCACGCCAC  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011520.5 (Graphical View of this Entry)  
 Chromosome : 22  
 map :  
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
 Position in Sequence : 6211178 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_011520.5 20010417\_4  
 Amplified region : 6210416..6211580 in NT\_011520  
 size : 1165  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075465](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075465)

12/17/2001



# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : AAGCTCAAAG CCAACTGGTA G  
 BackwardPrimer : TATGTACGTT GAATCTCTGA GT



FOOTER

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST075466

General Information

JSNP ID : IMS-JST075466  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6176283	22	23428071

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075466](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075466)

12/17/2001

TCCTGAGTAG

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GCTACTGCAG CCTGATACTT CTYGGCTTAA GCCATCCTCT CACCCAGGC TCCTGAGTAG  
Observed : C/T  
3' Assay : TAGGACTGCA GGTGCAGCC ACCATGCACA GCTAATTTTA ATTTTATAA AGCGGGGTC  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

## Screened Sequence

Accession No. : NT\_011520.5 (Graphical View of this Entry)  
Chromosome : 22  
map  
Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
Position in Sequence : 6211140 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_011520.5.20010417\_4  
Amplified region : 6210416..6211580 in NT\_011520  
size : 1165  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

PCR Condition

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : AAGCTCAAAG CCAACTGGTA G  
BackwardPrimer : TATGTACGTT GAATCTCTGA GT



PCR Program

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGCAACGTG	TCTCTGACTG
BackwardPrimer	:	AGGAGCTCA	GGGAAAGTAG



# SNP Information for IMS-JST105102

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105102  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	838851	11	76960358

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_009304.3	genomic	PTPNM1	intron*1	Annotated	
NT_009304.3	genomic	GSTP1	intron*1	Annotated	

PCR Cycle Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : AAGCTCAAAG CCAACTGGTA G  
BackwardPrimer : TAAGTACGTT GAATCTCTGA GT



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075470](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075470)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075472

## General Information

JSNP ID : IMS-JST075472  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6175553	22	23427341

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075472](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075472)



NT\_011520.5

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TAGTTCATTT TGCAGACATC TATTATGGA AATACTCAGA GATTCAACGT ACATACCAGC  
 Observed : C/T  
 3' Assay : GACATTGACA GGTGAATGGC TGCACCCAG ATGTGGTTTG TTATTTTAT TATAAATATT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011520.5 (Graphical View of this Entry)  
 Chromosome : 22  
 map  
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
 Position in Sequence : 6210410 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_011520.5 20010417\_5  
 Amplified region : 6209753..6210602 in NT\_011520  
 size : 850  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR-CT "E633609T"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CACCTCTCTA GCACTCACTG  
BackwardPrimer : ACAGGCATGC ATGCAAACTC



SNP Information



SNP Information for IMS-JST075473

General Information

SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

JSNP ID : IMS-JST075473

dbSNP ID(rs#) :

dbSNP ID(ss#) :

HGASE ID :

Organism : Homo sapiens

Molecular type : Genomic

Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN

Citation : J Hum Genet. 2001;46(4):225-40

Release Date : 2001/06/11

Last Update : 2001/06/11

Keyword

search

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6175202	22	23426990

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CACCTCTCTA GCACCTCACTG  
BackwardPrimer : ACAGGCATGC ATGCAAACTC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075473

General Information

JSNP ID : IMS-JST075473  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HCBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6175202	22	23426990

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

NT\_011520.5

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence : Information  
 5' Assay : CACTGTCTC AGCCAAGGGC CCAGCAGTGG CTCTCTGGG GTCTCCTTAA AAGGTGGCTC  
 Observed : G/T  
 3' Assay : CTGCCCTGG CTTGCCCGAG GCTATGGGTC GGACGTTCTT GGAGTAAAGC CTGACTTTAT  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011520.5 (Graphical View of this Entry)  
 Chromosome : 22  
 map  
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
 Position in Sequence : 6210059 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_011520.5.20010417\_5  
 Amplified region : 6209753..6210602 in NT\_011520  
 size : 850  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

--- SNP INFORMATION ---

SNP ID: 66666666

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CACCTCTCTA GCACCTGACTG  
BackwardPrimer : ACAGGCATGC ATGCAAACTC



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075473](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075473)

12/17/2001

# SNP Information for IMS-JST075475

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST075475  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6172975	22	23424763

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075475](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075475)

12/17/2001



TTGAGGCTTTTCTGGGAGCAGT

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CAGCTACTTG GGAGGCTGAG GCAGGAGAAAT CGCTTGACCC TGGGAGGCAG AGGTGCGCAGT  
 Observed : G/A  
 3' Assay : AGCTGAGATC ACGCCGTTGC ACTGTAGCCC GAGGACACAGA GCGAGACTCC ATCTCAAAAA  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011520.5 (Graphical View of this Entry)  
 Chromosome : 22  
 Map :  
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
 Position in Sequence : 6207832 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_011520.5\_20010417\_6  
 Amplified region : 6207648..6208318 in NT\_011520  
 size : 671  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075475](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075475)

12/17/2001

# PCR program

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : AGGTGGATGG GTGGATGACT  
BackwardPrimer : GAAGACGAAG TGAGAGGCTG CT



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075475](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075475)

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

Search

SNP Information for IMS-JST105079

General Information

JSNP ID : IMS-JST105079  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004966.5	3449967	1	114252371
NT_004966.5	3655834	1	114046504

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_004698.3	genomic	GSTM2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105079](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105079)

12/17/2001

NT\_004698.3

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CTGGAACATC CCGGGGTGA GCSAGGTTC GCTGGGGCGT GGGACGGGG TCGTGGGG  
 Observed : C/T  
 3' Assay : GGGGAAGTGT GGAGCACTG CAGGACGGC TCTAGGGACG GTTCCTCTTC AGGGCTGTCC  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_004698.3 ([Graphical View of this Entry](#))  
 Chromosome : 1  
 map  
 Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.  
 Position in Sequence : 3977 ([View SNP position in this record](#))

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_004698.3.20010416.1  
 Amplified region : 3344..4446 in NT\_004698  
 size : 1103

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105079](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105079)

12/17/2001

PCR Conditions

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGCTGATAAG TGACAGTGAG	
BackwardPrimer	:	CCAGCATTCT GCCTTGCAAG	



# SNP Information for IMS-JST105080

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

## General Information

JSNP ID : IMS-JST105080  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004966.5	3449104	1	114253234
NT_004966.5	3654971	1	114047367

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_004698.3	genomic	GSTM2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105080](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105080)

12/17/2001

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GGGGAAGGGG CGGTTTGGG GGAAAGTGG ACGTGTCTCT GACTGCATCT CCTCTCCCCA  
 Observed : G/C  
 3' Assay : CTTAGAGGTG TTAAGATCAG GAGTCTTCTG CCAATTCTCT CTCACTCTTG GCTGTCTACA  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_004698.3 (Graphical View of this Entry)  
 Chromosome : 1  
 map :  
 Definition of the record : Homo sapiens chromosome 1 working draft sequence  
 e segment.  
 Position in Sequence : 4840 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_004698.3.20010416.2  
 Amplified region : 4010..5234 in NT\_004698  
 size : 1225

PCR Program

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TAGGGACGGT TCCTCTTCAG	
BackwardPrimer	:	ATTCACTCTC AGCCTCACAG	





# SNP Information for IMS-JST105102

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105102  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	838851	11	76960358

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_009304.3	genomic	PTPNM1	intron*1	Annotated	
NT_009304.3	genomic	GSTP1	intron*1	Annotated	

# TOGETHER

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GAGATCCGAA CCCCTTATC CCTCCGTCGT GTGGCTTTTA CCCCCGGCCT CCTTCCGTGT  
Observed : C/T  
3' Assay : CCCGCCTCTC CCGCATGCC TGTCCCCCGC CCCAGTGTG TGTGAATCT TCGGAGGAAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_009304.3 ([Graphical View of this Entry](#))  
Chromosome : 11  
map :  
Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.  
Position in Sequence : 262297 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_009304.3.20010416.3  
Amplified region : 261152..262439 in NT\_009304  
size : 1288

PCR Conditions

Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CAGTTCGAGG TAGGACATG T  
BackwardPrimer : TTACTTGGCT GGTIGATGTC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105108

## General Information

JSNP ID : IMS-JST105108  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CCCAGCCCTG AGACAGGCCG CCCGCCGCC GCAATTGGAC TAAAGAGTGT CCCAGGCGTC  
 Observed : C/T  
 3' Assay : GTGCCGCCCA ATGGGCACA GCGGTCGGG TCGTAGCCG CAGGGCGGTG GTCTGAGGTC  
 Comment :  
 Sample size : 96

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105108](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105108)

12/17/2001

## Screened Sequence

Accession No. : AF240786.1 (Graphical View of this Entry)  
 Chromosome : 22  
 map : 22q11.2  
 Definition of the record : Homo sapiens glutathione S-transferase theta 2  
 (GSTT2) and glutathione S-transferase theta 1 (  
 GSTT1) genes, complete cds.  
 Position in Sequence : 93402 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : AF240786.1.20000829\_1  
 Amplified region : 92512..93729 in AF240786  
 size : 1218

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AGGACTCTGC AGTGTGAGC	
BackwardPrimer	:	AATGCAGACT GGACGAGTGC	

12/17/2001

# Footnote



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105108](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105108)

12/17/2001

# SNP Information for IMS-JST105152

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105152  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004648.5	2323162	1	165039379

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CTTCCAGCAG ATGCTTCTGT AGTATGTGAG GTTGAGAAA AGTCGATTG TGGTCATGTA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105152](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105152)

12/17/2001

NT\_004648.3 "CE33E00T"

Observed : G/T  
 3' Assay : GTATAGTCAT GCCACAGTGA TGAATAATTA AAGAAAAATC TTCTAGCTCT CAGGATATGC  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_004648.3 (Graphical View of this Entry)  
 Chromosome : 1  
 map  
 Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.  
 Position in Sequence : 399437 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_004648.3.20010416.8  
 Amplified region : 399374..400110 in NT\_004648  
 size : 737

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCAAAGGTCC TAGAGCAAG T	



TOPSITE = 66882007

BackwardPrimer : AATGCATATC CTGAGAGCTA G



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105152](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105152)

12/17/2001

# SNP Information for IMS-JST104848

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST104848  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_028388.2	301178	19	71733798

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011148.3	genomic	NDUFA3	CDS*1	Annotated	

NT\_011148.3

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GGGAACATGC CCGACGTGCC CAGCCACCCC CAGGAYCCTC AGGGCCCCAG CCTGGAGTGG  
 Observed : C/G  
 3' Assay : TGAAGAACT GTGAGCACCT CCACTGACAG AGGGGGCCCC TCCCACGGCT CCCAATAAAA  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011148.3 ([Graphical View of this Entry](#))  
 Chromosome : 19  
 map  
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
 Position in Sequence : 281924 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_011148.3.20010417.3  
 Amplified region : 281625..282277 in NT\_011148  
 size : 653  
 pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP\\_ID=IMS-IST104848](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-IST104848)

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TCTTGGTCTC CATCTTCTCA G  
BackwardPrimer : GTTCCTTATC TCCTGCAGAT



# SNP Information for IMS-JST104850

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST104850  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_028388.2	300086	19	71732706

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : AACTCAGCCC CAGCCCTGGC CCTCCCTT GAGTCCCCC TCCTACCTG CACTGGCACC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104850](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104850)

12/17/2001

TCCTGGAGC CCCAGTCCCT CCCCTTGACT TCCCGCCTTC CTCACCTGCA CCGGGGCCAG

Observed : A/G  
3' Assay : GCTCTGGAGC CCCAGTCCCT CCCCTTGACT TCCCGCCTTC CTCACCTGCA CCGGGGCCAG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_011148.3 (Graphical View of this Entry)  
Chromosome : 19  
map :  
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
Position in Sequence : 280831 ([View SNP position in this record](#))

### Method

[PCR Method](#)  
[Sequence Method](#)

### PCR Profile

Screening region ID : NT\_011148.3.20010417.4  
Amplified region : 280322..281257 in NT\_011148  
size : 936

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CACAGTTCTT GTCTGCCAG	

TTGAGTGGAG TGGGAGCTGA

BackwardPrimer : TTGAGTGGAG TGGGAGCTGA



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST104850](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST104850)

104247 44834004

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST104853

General Information

JSNP ID : IMS-JST104853  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007933.5	5088316	7	121644918

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_025775.1	genomic	NDUFA5	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104853](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104853)

12/17/2001



102427 653600

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : ATTTTCATCT TAGTTCTAAT ACTTATTGT GGAGTGACTT GGATATTGC TAGTTTCTC  
 Observed : G/T  
 3' Assay : GTCTCAATTT CATCATCTAT AACGTGGGTA TAATAATACC CACCTCGAAC ACTTTTGT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_025775.1 ([Graphical View of this Entry](#))  
 Chromosome : 7  
 map  
 Definition of the record : Homo sapiens chromosome 7 working draft sequence segment.  
 Position in Sequence : 17431 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_025775.1.20010416.2  
 Amplified region : 17117..17737 in NT\_025775  
 size : 621  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycle # E63E00T

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : GTCTTTATCC CAAAGGCTAG  
BackwardPrimer : TCACTGTTAT AAGAGACTCA G



# SNP Information for IMS-JST104864

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BIAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST104864  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HCBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

Keyword



## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027196.2	24630	19	10190164

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CCAAAACCTC TCACCCCTGGG CTTAACGAAG CCTCCCTACC ACCAACCAAA GGTCTATCAA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104864](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104864)

12/17/2001

CCGCGGCTTCT

Observed : A/G  
3' Assay : GGGGTGTCCT CTTTGCACCC ACCAGCGAGC AGCCAAGCTC AGGCAACCT CCGGGCTTCT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_027196.1 (Graphical View of this Entry)  
Chromosome : 19  
map  
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
Position in Sequence : 254198 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_027196.1.20010716.1  
Amplified region : 254003..255052 in NT\_027196  
size : 1050

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCTCAAGGAG ATTGCAGCAG	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104864](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104864)

12/17/2001

TTACTTCTTC CTCACCTCCG

BackwardPrimer : TTACTTCTTC CTCACCTCCG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104864](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104864)

1042337 E886001

# SNP Information for IMS-JST104866

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST104866  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027196.2	24966	19	10189828

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_027196.1	genomic	RPS28	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104866](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104866)

12/17/2001

TCAGATTCCTGGG

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TAAAGGGAAC CATCAGAAC CYGTGATGAA ATGAGAAATCG GCTCCCCGGAT TCCGGGTGGC  
 Observed : A/G  
 3' Assay : GGGGTTAGGG CAGGGTAGAG GTACATCAG GGTTAGGTC GCCGGCAGTC GCCCAAAATGC  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_027196.1 (Graphical View of this Entry)  
 Chromosome : 19  
 map  
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
 Position in Sequence : 253862 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_027196.1\_20010716\_2  
 Amplified region : 253200..254220 in NT\_027196  
 size : 1021  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CCACCAACCA AAGTCTATC  
BackwardPrimer : GAAATCCCAG GCCTGAGTG





TOGETHER

# SNP Information for IMS-JST104870

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST104870  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword



## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027196.2	25572	19	10189222

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_027196.1	genomic	NDUFA7	intron*1	Annotated	

## Allele Sequence

Variation Type	SNP
Flanking Sequence	Information
5' Assay	CTCCCTCCTA AGCCGGRACC CTTCGCTCTC CCGGAATCTC CCTGGGAACC CCCAGCTMGT
Observed	C/G
3' Assay	ACCCCTTCAG CCCGGGACCC TCTCCTGGCC TGGGAACCAAC TCAGGCCTGG GATTTCCCCCA
Comment	
Sample size	96

## Screened Sequence

Accession No.	:	NT_027196.1	(Graphical View of this Entry)
Chromosome	:	19	
map	:		
Definition of the record	:	Homo sapiens chromosome 19 working draft sequence segment.	
Position in Sequence	:	253256	(View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

```

Screening region ID : NT_027196.1.20010716.3
Amplified region   : 252841..253561 in NT_027196
size               : 721

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes

```

# PCR "CONDITIONS"

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : CCTTTATAGG ACGTTCTAGC  
 BackwardPrimer : ATGTCAGCCC TCCGTTTCAG



# SNP Information for IMS-JST104892

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

## General Information

JSNP ID : IMS-JST104892  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	821019	12	4611354

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TAGATGGCTC TTGTGTAGAAC AAKGCAGATT CTCAAAGGTG ACCACAGTTA AAGAAAAAT

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104892](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892)

Observed	:	T/C
3' Assay	:	ACAAGCATT GCGTAGAGA GAGCATCTCG CAGTTCTCC TTAGACAGAT GTTCAGATGG
Comment	:	
Sample size	:	96

## Screened Sequence

```

Accession No.      : NT_024413.3 (Graphical View of this Entry)
Chromosome         : 12
map                :
Definition of the record : Homo sapiens chromosome 12 working draft sequence segment.
Position in Sequence : 536287 (View SNP position in this record)

```

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID	:	NT_024413.3.20010417_1
Amplified region	:	536137..536950 in NT_024413
size	:	814
Pre-Denature	:	94.0 degrees C for 2.00 minutes
Denaturation	:	94.0 degrees C for 0.50 minutes
Annealing	:	60.0 degrees C for 0.50 minutes
Polymerization	:	72.0 degrees C for 2.00 minutes
PCR Cycles	:	35
Post-Extension	:	72.0 degrees C for 7.00 minutes
ForwardPrimer	:	CTGAGAACAT GAGGCAGTGT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104892](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892)

12/17/2001

TTGGTTTGGGGGGT

BackwardPrimer : GAGTTCCTTAA CCAGAACTGT G



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104892](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892)

# SNP Information for IMS-JST104894

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST104894  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	820603	12	4611770

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : ATGTGCTTGG CGGGCTCGAC GCACATTAT TTAATTGGGA CACACCTAT TTGGTTTCT

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104894](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104894)

# PCR "CONDITIONS"

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : GCTAGAAGTC CATTATCAGT C  
 BackwardPrimer : AGATTCCAT AATGTGGCAT G





TCGTTACAG CTGCTTAAGA T

BackwardPrimer : TCGTTACAG CTGCTTAAGA T



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST104894](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST104894)

FOR THE "CEEG001"

# SNP Information for IMS-JST104917

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST104917  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword



## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	806730	12	4625643

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104917](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104917)

12/17/2001

Top of the page

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GTCCTAATAG TGGAAAGAAT GGATGCTTTA TTCACCTTGC TCFAAACTCA AAACAGGTTT  
Observed : G/A  
3' Assay : TTTGGTTATT GTTAGGCTG TTGGAGAGAA AGTAGTGAGA GATGCAATTC CGGAAGCCAT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_024413.3 ([Graphical View of this Entry](#))  
Chromosome : 12  
map :  
Definition of the record : Homo sapiens chromosome 12 working draft sequence segment.  
Position in Sequence : 521998 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_024413.3.20010417.11  
Amplified region : 521231..522366 in NT\_024413  
size : 1136  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "REACT"

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTTCCATTAT TGCAGCCTGC	
BackwardPrimer	:	GATGTTAGGT GGACACAAGC A	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST104919

General Information

JSNP ID : IMS-JST104919  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	806093	12	4626280

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	

[illegible]

## Screened Sequence

## Method

## PCR Profile

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CTTCCATTAT TGCAGCCTGC  
BackwardPrimer : GATGTTAGGT GGACACAAGC A



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST104929

General Information

JSNP ID : IMS-JST104929  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	784948	12	4647425

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	



NT\_024413.3

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AGCTTCCTTT TTCAATTAAT TATACTATGC ATTAGAATGT TGTTTTCAA GCCTTTAAAC  
Observed : G/A  
3' Assay : GCTGTGAAC CCTGTGCTCA CTGAAGTTT ACCTCAAGTC CTGCTGGGTA AATCCAATAA  
Comment :  
Sample size : 96

Screened Sequence

Accession No. : NT\_024413.3 (Graphical View of this Entry)  
Chromosome : 12  
map :  
Definition of the record : Homo sapiens chromosome 12 working draft sequence segment.  
Position in Sequence : 500216 (View SNP position in this record)

Method

PCR Method  
Sequence Method

PCR Profile

Screening region ID : NT\_024413.3.20010417\_16  
Amplified region : 499336..500446 in NT\_024413  
size : 1111  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "CCTCT"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CTGAGGACAC TAGAATAGAG A  
BackwardPrimer : AGACAGACCG CTGTAGAGCA



FOOT" 6634007

# SNP Information for IMS-JST105055

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105055  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HCBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011151.5	21436	19	16971264

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011151.3	genomic	NDUFB7	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105055](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105055)

12/17/2001

NT\_011151.3 "CEB001"

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CCAGTGGCA GCGCAGCCA GAGGCGTGG GCGCGGGTG CCTGAACACC TGGCACCCCA  
 Observed : G/A  
 3' Assay : GGCTGGCACC CCAGGCGTGG GCTCTAACCT CAGGTGTTGT ATCTGGGTTT GGGTCTAGAC  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011151.3 (Graphical View of this Entry)  
 Chromosome : 19  
 map  
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
 Position in Sequence : 21436 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_011151.3.20010417.1  
 Amplified region : 20923..21598 in NT\_011151  
 size : 676  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycling Conditions

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TAGCCTCGGG CTACCAAGAAG	
BackwardPrimer	:	CTTGTCGCCT CACTTTTGCT	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST104938

## General Information

JSNP ID : IMS-JST104938  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGEASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1022576	2	202474233

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

TTGTTGTTGTTT

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence : Information  
 5' Assay : TGTTTGGTTCG CTGTTGTGTT AGCAATGGCT CACGCYTCG TTTGTTGTCC TTGTTTGT  
 Observed : G/T  
 3' Assay : GTCCATTGAC CACGTTGGAC AGCATTTTTT TRTTCTTTTA ACTAACGGGA AATTGAGAAA  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_005370.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map  
 Definition of the record : Homo sapiens chromosome 2 working draft sequenc  
 e segment.  
 Position in Sequence : 450299 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_005370.2.20010209\_1  
 Amplified region : 449472..450696 in NT\_005370  
 size : 1225  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP\\_ID=IMS-IST104938](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-IST104938)

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TCTTAAGTTC GTACCTCCAC G  
BackwardPrimer : GACTCATTC TGGCTCGTAG





# SNP Information for IMS-JST104943

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST104943  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1032841	2	202463968

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104943](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104943)

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TGATCATTCG GTATTGTTAA AACTTACAAT TTTCTTTATT TTITGAAACG AGGTCTCACT  
Observed : A/G  
3' Assay : TGTTCCTCCAG GCTGGGCTTG AACTCCTGGC CTCAGGTGAT CATCCTGCCT CAGCCCTCCCT  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

### Screened Sequence

Accession No. : NT\_005370.2 (Graphical View of this Entry)  
Chromosome : 2  
map  
Definition of the record : Homo sapiens chromosome 2 working draft sequence  
Position in Sequence : 460564 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_005370.2\_20010209\_4  
Amplified region : 459433..460769 in NT\_005370  
size : 1337  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : ATATCGTAGT GGAGAACCTA G  
BackwardPrimer : CTCGCCGAGTA TCATTCTGGT A



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104943](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104943)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST104944

General Information

JSNP ID : IMS-JST104944  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1038241	2	202458568

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104944](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104944)

12/17/2001

NT\_005370.2

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GTGTTTGA GATGGAGTTT TGCTGTTGTC GCCCAGGCTG GAGTCCGCTG GCGCGATCTC  
 Observed : G/A  
 3' Assay : ATCTGGGTC ACTGCAGCCT CTGCCTCCTT GGTCAAGCA GTTCTCCTGC CTCATCCTCC  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_005370.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map :  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 465964 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_005370.2.20010209.5  
 Amplified region : 465711..467023 in NT\_005370  
 size : 1313  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104944](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104944)

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : AGATACTTCA GAGGAGTCG  
BackwardPrimer : ATCAAAACCCA TTGCCTTCTC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST104947

## General Information

JSNP ID : IMS-JST104947  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HCBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1039346	2	202457463

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NIDUFS1	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GGCAATGGGT TTGATGATAG GAGAATATTT CATGGATCT CTGTATGCT TAAATTTAAA  
 Observed : G/T  
 3' Assay : TAAATTGCA TTTTATATAT TGTATTCTTA GCACAGATTT GCGTTCCAAT TATCTTCTTA  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_005370.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 467069 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_005370.2\_20010209\_6  
 Amplified region : 466599..468073 in NT\_005370  
 size : 1475  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes



Variable	Mean	Standard deviation	Minimum	Maximum
Age (years)	34.5	10.5	18	65
Gender (male/female)	10/10			
Marital status (single/married)	10/10			
Education (years)	12.5	1.5	9	16
Occupation (student/worker)	10/10			
Religion (Muslim/Hindu)	10/10			
Family size (children)	2.5	1.5	0	5
Income (Rs. per month)	10,000	5,000	5,000	20,000
Health status (good/poor)	10/10			
Smoking status (yes/no)	10/10			
Alcohol consumption (yes/no)	10/10			
Exercise frequency (times/week)	2.5	1.5	0	5
Dietary habits (vegetarian/non-vegetarian)	10/10			
Stress level (low/high)	10/10			
Sleep quality (good/poor)	10/10			
Work-life balance (satisfied/dissatisfied)	10/10			
Overall health satisfaction (satisfied/dissatisfied)	10/10			

Annealing	:	60.0 degrees C for 0.50 minutes
Polymerization	:	72.0 degrees C for 2.00 minutes
PCR Cycles	:	35
Post-Extension	:	72.0 degrees C for 7.00 minutes

ForwardPrimer : AGACCAAGAT CAAACCAGAA G  
BackwardPrimer : AAGGAGAGGA GAAAACGGAC



12/17/2001

# SNP Information for IMS-JST104949

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST104949  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1048121	2	202448688

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

NT\_005370.2

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CTGACCACAG GATAATTTGC TAGGCTTTT ATTCTGAATA ATTACTTTTA GAAAACGTGT  
 Observed : T/C  
 3' Assay : TTAGCTGATA CTCAGGCATA TTTCACAGTA GCATTGGCAA GATGCTTTGG ATTAAACTAA  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_005370.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 475844 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_005370.2.20010209\_7  
 Amplified region : 475669..476952 in NT\_005370  
 size : 1284  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104949](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104949)

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : GTAGATGGAA GATAGTAGGC A  
BackwardPrimer : AGGATCAGTT CCATTCTGC AC



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104949](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104949)

12/17/2001

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

# SNP Information for IMS-JST104958

## General Information

JSNP ID : IMS-JST104958  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1057719	2	202439090

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GGGTAAATAG GAAAAATACA TAATCATGCT CAGATATGTA TCTAGGATAA TTATAATTAA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104958](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104958)

12/17/2001

TTAGCTTTA CTAATGATGTA

Observed : T/A  
3' Assay : AATAATCATA GTAACAATGG CTAATGATGTA TTAGCTTTA TTATATGTGC TAAGCACTCT  
Comment : repeat sequence (repeat sequence exists in flanking sequence)  
Sample size : 96

## Screened Sequence

Accession No. : NT\_005370.2 (Graphical View of this Entry)  
Chromosome : 2  
map  
Definition of the record : Homo sapiens chromosome 2 working draft sequence  
Position in Sequence : 485442 ([View SNP position in this record](#))

## Method

[PCR Method](#)  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_005370.2.20010209\_11  
Amplified region : 484655..485807 in NT\_005370  
size : 1153

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extention	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GCATACTGGT GCACGTGCTA	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104958](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104958)

12/17/2001

BackwardPrimer : ACCATGACAT TATAGAAGCA GA



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104958](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104958)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



General Information

JSNP ID : IMS-JST104960  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008978.5	308976	11	46472116

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_008956.3	genomic	MTCH2	intron*1	Annotated	
NT_008956.3	genomic	NDUFS3	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104960](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104960)

12/17/2001



For "CECCE001"

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CGGCGCTGAC CAGGGGTGAG CACGGGCAGC CAGCTGAGAC CGGGGTGAGG CGCAGCGGCG  
Observed : T/C  
3' Assay : GCCCAGTGCA GAGAGCTCCT CAGGGCTCAT CCGCGCGCTC TGTGCCCTTT ATCTCCCTGT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_008956.3 (Graphical View of this Entry)  
Chromosome : 11  
map :  
Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.  
Position in Sequence : 737571 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_008956.3.20010416.2  
Amplified region : 736668..737858 in NT\_008956  
size : 1191

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104960](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104960)

12/17/2001

PCR Conditions

Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TGTCTCGCTT TCTCACTGC  
BackwardPrimer : CTTGAAGATC CCTCACAGAC



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104960](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104960)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## SNP Information for IMS-JST104978

### General Information

JSNP ID : IMS-JST104978  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

### Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006693.5	251179	5	48905237

### Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006693.3	genomic	NDUFS4	intron*1	Annotated	

TOP SECRET

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTTAATAGAC AAATTCTCTCA ACTGATAATT CAAAGTTCTT CACAATATAG GCACAAACTT  
Observed : A/C  
3' Assay : CTACCAAAGC ACTAACAAGT TTTGTCTCTG TTCCAACCTCT TACTTCTGC CCTTACATTG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_006693.3 (Graphical View of this Entry)  
Chromosome : 5  
map  
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.  
Position in Sequence : 754982 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_006693.3.20010416\_9  
Amplified region : 754001..755125 in NT\_006693  
size : 1125  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : ACTGTTACGT ATACTGCCTC A  
BackwardPrimer : ACTAGCATCA TAGTACCAGG A



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST104978](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST104978)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST104980

## General Information

JSNP ID : IMS-JST104980  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006693.5	253052	5	48907110

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006693.3	genomic	NDUFS4	intron*1	Annotated	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104980](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104980)

TOP SECRET

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence : Information  
 5' Assay : TACACAGTT CCCCCATTAA TCATCTGTTT TCAGTIGITA ACCAAATAAG GTATTATGCA  
 Observed : G/A  
 3' Assay : GGTCACTCTT TTATATAAGA ATACTCTACT CTTGTTTTTG AGATGAAAAG AAGTTCTCTT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006693.3 (Graphical View of this Entry)  
 Chromosome : 5  
 map  
 Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.  
 Position in Sequence : 753109 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_006693.3\_20010416\_10  
 Amplified region : 752239..753543 in NT\_006693  
 size : 1305  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104980](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104980)

PCR "SEQUENCE"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TCTTCAGGTA CTCTTACCTA G  
BackwardPrimer : CGTGCCTTCTA CCTTCTATTA C



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104980](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104980)



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST104982

## General Information

JSNP ID : IMS-JST104982  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006693.5	259294	5	48913352

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006693.3	genomic	NDUFS4	intron*1	Annotated	

TOGETHER

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ACCTTATTG CTTGTTTAA TCACTTTATA TAAATTTTCAAT GGAAGACTT GCTTTGCCAG  
Observed : T/C  
3' Assay : GTATCCGAAA CCTCTGTTAT TTCTCCATAG TATTTTCTAT AGAAGATCTA GGATACTTTT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006693.3 (Graphical View of this Entry)  
Chromosome : 5  
map  
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.  
Position in Sequence : 746867 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006693.3 20010416\_11  
Amplified region : 746420..747407 in NT\_006693  
size : 988  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST104982](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST104982)

PCR PROGRAM

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCCTGGATCC TGCTGTAGC  
BackwardPrimer : CTGACATGAG TTGGGAAGTG A



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST104982](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104982)

12/17/2001

# SNP Information for IMS-JST105004

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105004  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword



## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004893.5	9766	1	39174537

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AGTAGTTCTA CTATAAAGGA ACTCATTTAA CTTTGCTTAA CCCAACAGCT CCCAATGTAA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105004](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105004)

12/17/2001

TGAGGTTTGGGGT

Observed : A/G  
 3' Assay : ACAGATCTAT TAATATTCTG AGGAACCCAG TTGTATGGGT CACCAGACTA GGAACAATA  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_004893.3 (Graphical View of this Entry)  
 Chromosome : 1  
 map  
 Definition of the record : Homo sapiens chromosome 1 working draft sequence  
 e segment.  
 Position in Sequence : 969241 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_004893.3 20010416\_6  
 Amplified region : 968721..969831 in NT\_004893  
 size : 1111

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGGGATGGC TAGAAAGCTA	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105004](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105004)

12/17/2001

TGCTAAAC TCTCAACAGG T

BackwardPrimer : TGCTAAAC TCTCAACAGG T



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105004](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105004)

# SNP Information for IMS-JST105012

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105012  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

Keyword



## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004893.5	42727	1	39141576

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TGCAATTGGCA CGATCTTGGC TCACTGCAAC CACCATCTCC CAGATTCAAG TGGTTCTCCT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105012](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105012)

12/17/2001

TAAGTATTTT

Observed : G/C  
3' Assay : CCTCAGCCTC CCAAGTAGCT GGGACTACAG GCATGCACCA CCACACCCAG CTAATTTTTC  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

### Screened Sequence

Accession No. : NT\_004893.3 (Graphical View of this Entry)  
Chromosome : 1  
map  
Definition of the record : Homo sapiens chromosome 1 working draft sequence  
e segment.  
Position in Sequence : 958402 ([View SNP position in this record](#))

### Method

[PCR Method](#)  
[Sequence Method](#)

### PCR Profile

Screening region ID : NT\_004893.3 20010416\_10  
Amplified region : 958036..958985 in NT\_004893  
size : 950

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TCAGAGAGGT TATGTATACT	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105012](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105012)



TTCTTTT

BackwardPrimer : AACACTATCA TTCTTAAAT GAG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105012](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105012)

12/17/2001



NT\_006455.3

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GCACTGAGCT CCTGGAGCCA GACGTTTGCT GGTGATGGC GGTGAGGTC ACCCTTGAGC  
Observed : T/C  
3' Assay : GCGCACACTA AATGACGGGA GGGCATCCG CGTCAGTCRC CAGTGTCGAG GCGTCAGCAG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_006455.3 ([Graphical View of this Entry](#))  
Chromosome : 5  
map  
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.  
Position in Sequence : 219541 ([View SNP position in this record](#))

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_006455.3\_20010416\_4  
Amplified region : 219323..220443 in NT\_006455  
size : 1121  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR REACTION

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : ATCCACAT TCTCAAAGCA AG  
BackwardPrimer : CTGCTGCAGG CGATGCAACT



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105024](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105024)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



General Information

JSNP ID : IMS-JST105029  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029292.1	194050	5	63449263

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006455.3	genomic	NDUFS6	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105029](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105029)

12/17/2001

NT\_006455.3

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TACAGCGCCA CACTACAGGG CCTACATAGA GCGGCCTGTC CGAARACCCC CTTTCAACTG  
Observed : T/C  
3' Assay : GAAAGTGGTGG GCGGCATGTT TCTCTTCTCG GACGCCCAAG CGTCITTCCT CTCTGGGCCC  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_006455.3 (Graphical View of this Entry)  
Chromosome : 5  
map :  
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.  
Position in Sequence : 214432 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_006455.3\_20010416\_7  
Amplified region : 213959..214961 in NT\_006455  
size : 1003  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GCGTTTGGAA CTTTATTCCA GT  
BackwardPrimer : GTCCTGTATA TGACACTCAT C



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105029](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105029)

# SNP Information for IMS-JST105030

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

## General Information

JSNP ID : IMS-JST105030  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029292.1	193227	5	63448440

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006455.3	genomic	NDUFS6	intron *1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105030](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105030)

12/17/2001



T O A G T T G G G G G G T

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GAAAAGGGGA CAGTCTAACA GGCATAAATG GTTAAGCAGC CTAGAGTGGG ACTGGGCACC  
Observed : C/T  
3' Assay : GGCATGTCCC CTCCTGGGCT CCAGCCCTGA AGGCCAAGCC TGGTTGTGCC TCACTGTTCGT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006455.3 (Graphical View of this Entry)  
Chromosome : 5  
map :  
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.  
Position in Sequence : 213609 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006455.3\_20010416.8  
Amplified region : 212603..213807 in NT\_006455  
size : 1205  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105030](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105030)

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CACCGACAGT GGAGCACTCA G  
BackwardPrimer : ATGTGACTTT CGATGCTTC A



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105030](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105030)

# SNP Information for IMS-JST105031

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105031  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029292.1	192402	5	63447615

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GGAGAAGGAG AAGTGCCTCT TGTTTTGCAG ATGCAACTGT GCTTCAGAGA GCCAAGGTGG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105031](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105031)

12/17/2001

# FOXP1 "E63600"

Observed : A/G  
3' Assay : ATGTGACCTC TCCACATTC TCCGGTGCTG TGATGTACCT TAAACACAGC AAGGTACTTG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 (Graphical View of this Entry)  
Chromosome : 6  
map  
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
Position in Sequence : 183417 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_026300.1\_20010416\_4  
Amplified region : 182827..184053 in NT\_026300  
size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

Sequence

BackwardPrimer : ATGTGACTTT CGATGCTTC A



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105031](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105031)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

## General Information

JSNP ID : IMS-JST105033  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	1341784	11	76457425

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CCCCCTGGCT CACTCAGGAT CCGGGGCCCTC CGTGTCCTTC AGGTGCAGCG GGGAGCCGGC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105033](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105033)

12/17/2001

TOGETHER

Observed : T/C  
 3' Assay : CTCAGGGCGC ATGCGCGCC CGTCTGTGGC CACCGGCCTA GTTAGGTCG GAGATCACTG  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_008940.3 (Graphical View of this Entry)  
 Chromosome : 11  
 map  
 Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.  
 Position in Sequence : 752973 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_008940.3\_20010416\_1  
 Amplified region : 752610..753519 in NT\_008940  
 size : 910

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymorization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	ATCTCGTCGC	CATTACCGTC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105033](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105033)

12/17/2001

TCCTCGGTA CCACATTCCT

BackwardPrimer : GTCTCGGTA CCACATTCCT



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105033](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105033)



# SNP Information for IMS-JST105036

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105036  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	1343347	11	76455862

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_008940.3	genomic	NDUFS8	intron*1	Annotated	

NT\_008940.3

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GAGACCTGAG TTCCAGTCC TGGCTTGTCA GGGGCGTTCT TCTCTGAGCC TGTTCCTCACT  
Observed : T/C  
3' Assay : TTAAATGAT TATGGTGATG GAGACTGACT CTGATTCA GGGCAGGGT CCATCATTGC  
Comment : repeat sequence (repeat sequence exists in flanking sequence)  
Sample size : 96

### Screened Sequence

Accession No. : NT\_008940.3 ([Graphical View of this Entry](#))  
Chromosome : 11  
map  
Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.  
Position in Sequence : 751410 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_008940.3\_20010416\_2  
Amplified region : 751038..752167 in NT\_008940  
size : 1130  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GGAGTCCTTG TAAGATAGG A  
BackwardPrimer : GGTCGCAACTG CTGGGCTACA



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105036](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105036)

TOGETHER

# SNP Information for IMS-JST105043

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

## General Information

JSNP ID : IMS-JST105043  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	1349122	11	76450087

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CCAGGCCCGG CTCTGGGGGT CCACTTGTC ACCCTGCCG CAGCCACACA GGCCTGTGCT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105043](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105043)

12/17/2001

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	1500	500	1000	2500
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Depression score	0.5	0.5	0	1
Anxiety score	0.5	0.5	0	1
Quality of life	0.5	0.5	0	1
Physical health	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Emotional health	0.5	0.5	0	1
Behavioral health	0.5	0.5	0	1
Environmental health	0.5	0.5	0	1
Occupational health	0.5	0.5	0	1
Financial health	0.5	0.5	0	1
Family health	0.5	0.5	0	1
Community health	0.5	0.5	0	1
National health	0.5	0.5	0	1
Global health	0.5	0.5	0	1
World health	0.5	0.5	0	1
Universal health	0.5	0.5	0	1
Human health	0.5	0.5	0	1
Planetary health	0.5	0.5	0	1
Ecosystem health	0.5	0.5	0	1
Biodiversity health	0.5	0.5	0	1
Climate health	0.5	0.5	0	1
Environmental quality	0.5	0.5	0	1
Air quality	0.5	0.5	0	1
Water quality	0.5	0.5	0	1
Soil quality	0.5	0.5	0	1
Land use	0.5	0.5	0	1
Urbanization	0.5	0.5	0	1
Ruralization	0.5	0.5	0	1
Deforestation	0.5	0.5	0	1
Reforestation	0.5	0.5	0	1
Conservation	0.5	0.5	0	1
Development	0.5	0.5	0	1
Growth	0.5	0.5	0	1
Progress	0.5	0.5	0	1
Success	0.5	0.5	0	1
Failure	0.5	0.5	0	1
Victory	0.5	0.5	0	1
Defeat	0.5	0.5	0	1
Triumph	0.5	0.5	0	1
Setback	0.5	0.5	0	1
Progression	0.5	0.5	0	1
Regression	0.5	0.5	0	1
Advancement	0.5	0.5	0	1
Retardation	0.5	0.5	0	1
Acceleration	0.5	0.5	0	1
Deceleration	0.5	0.5	0	1
Stabilization	0.5	0.5	0	1
Fluctuation	0.5	0.5	0	1
Stability	0.5	0.5	0	1
Instability	0.5	0.5	0	1
Consistency	0.5	0.5	0	1
Inconsistency	0.5	0.5	0	1
Uniformity	0.5	0.5	0	1
Non-uniformity	0.5	0.5	0	1
Equality	0.5	0.5	0	1
Inequality	0.5	0.5	0	1
Justice	0.5	0.5	0	1
Injustice	0.5	0.5	0	1
Fairness	0.5	0.5	0	1
Unfairness	0.5	0.5	0	1
Integrity	0.5	0.5	0	1
Lack of integrity	0.5	0.5	0	1
Honesty	0.5	0.5	0	1
Dishonesty	0.5	0.5	0	1
Truthfulness	0.5	0.5	0	1
Untruthfulness	0.5	0.5	0	1
Reliability	0.5	0.5	0	1
Unreliability	0.5	0.5	0	1
Trustworthiness	0.5	0.5	0	1
Untrustworthiness	0.5	0.5	0	1
Accountability	0.			

Observed	:	C/A
3' Assay	:	GCTGTGTGGG GCTTAGGGAT CACCAGRGCT GAAGGGCCCC TGGCCTCCAG TGGGAATGCC
Comment	:	
Sample size	:	96

## Screened Sequence

Accession No.	:	NT 008940.3	(Graphical View of this Entry)
Chromosome	:	11	
map	:		
Definition of the record	:	Homo sapiens chromosome 11 working draft sequence segment.	
Position in Sequence	:	745636	(View SNP position in this record)

## Method

<u>PCR Method</u>	<u>Sequence Method</u>
98.7%	96.0%

# PCR Profile

Screening region ID	:	NT_008940.3	20010416_5
Amplified region	:	745238..746342	in NT_008940
size	:	1105	
Pre-Denature	:	94.0 degrees	C for 2.00 minutes
Denaturation	:	94.0 degrees	C for 0.50 minutes
Annealing	:	60.0 degrees	C for 0.50 minutes
Polymerization	:	72.0 degrees	C for 2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees	C for 7.00 minutes
ForwardPrimer	:	CCAGTCAGTGT	TTGGAATGC T

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105043](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105043)

12/17/2001

T O A G T T G G G C C C T

BackwardPrimer : GGTGCTTACA CCTTCCTGCT



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105043](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105043)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075272  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40.  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	681007	6	2980483

Gene Information

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GCAACTCCTA GAGGGGTCCT TGGGGAGACG CGGGTCCCAG TCCTGGGGCT CCTACTGGGG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075272](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075272)

12/17/2001

Observed	:	A/C
3' Assay	:	GTCCGCTGGT CGGAAGGTGA GTGATCCCT GTCGGGACC GGGGACTTG GGAAGGACAG
Comment	:	
Sample size	:	96

```

Accession No.      : NT_026300.1 (Graphical View of this Entry)
Chromosome        : 6
map              :
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 187084 (View SNP position in this record)

```

PCR Method  
Sequence Method

Screening region ID	:	NT_026300.1.20010416_2	
Amplified region	:	186698..187589 in NT_026300	
size	:	892	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TATCAATCCA GTTTCACCT	G

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075272](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075272)

12/17/2001



TGGGTTTCCGCGCT

BackwardPrimer : CAGCGCAAC CAGTGGTTCA



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075272](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075272)

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075273

## General Information

JSNP ID : IMS-JST075273  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	682942	6	2978548

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTCCCCACT ATTCAAATA GTATAGAAA TAGAGCTGAG TCACTCAAT AGAGCTGAGT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075273](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075273)

12/17/2001

Observed	:	T/C
3' Assay	:	AGTCACTCAG CTCCTGGACC TCAGATTCCTT ATTCCTAACC GCTAGGGGGA TGGAGACAGA
Comment	:	
Sample size	:	96

```

Accession No.      : NT_026300.1 (Graphical View of this Entry)
Chromosome         : 6
map                :
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 185149 (View SNP position in this record)

```

PCR Method  
Sequence Method

Screening region ID	:	NT_026300.1_20010416_3
Amplified region	:	184926..185711 in NT_026300
size	:	786
Pre-Denature	:	94.0 degrees C for 2.00 minutes
Denaturation	:	94.0 degrees C for 0.50 minutes
Annealing	:	60.0 degrees C for 0.50 minutes
Polymerization	:	72.0 degrees C for 2.00 minutes
PCR Cycles	:	35
Post-Extension	:	72.0 degrees C for 7.00 minutes
ForwardPrimer	:	ATCTCGAAG ATCACAGCCA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075273](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075273)

TGGTTTGGGGT

BackwardPrimer : AGTGATTGCC CGAAATCATG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075273](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075273)

12/17/2001

# SNP Information for IMS-JST075274

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075274  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Keyword

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	683027	6	2978463

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ATTCTTATTC TTAACCGCTA GGGGGATGGA GACAGAAGTC ACAAACTCAC ATGCCACCAG

10036633 100304

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST075584

General Information

JSNP ID : IMS-JST075584  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	419468	4	68119470

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																																
Population (millions)	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4.0	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5	7.6	7.7	7.8	7.9	8.0	8.1	8.2	8.3	8.4	8.5	8.6	8.7	8.8	8.9	9.0	9.1	9.2	9.3	9.4	9.5	9.6	9.7	9.8	9.9	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4

Accession No.	:	NT_026300.1	(Graphical View of this Entry)
Chromosome	:	6	
map	:		
Definition of the record	:	Homo sapiens chromosome 6 working draft sequence segment.	
Position in Sequence	:	185064	(View SNP position in this record)

<u>PCR Method</u>	
Sequence Method	

Screening region ID	:	NT_026300.120010416_3
Amplified region	:	184926..185711 in NT_026300
size	:	786
Pre-Denature	:	94.0 degrees C for 2.00 minutes
Denaturation	:	94.0 degrees C for 0.50 minutes
Annealing	:	60.0 degrees C for 0.50 minutes
Polymerization	:	72.0 degrees C for 2.00 minutes
PCR Cycles	:	35
Post-Extension	:	72.0 degrees C for 7.00 minutes
ForwardPrimer	:	ATCTCCGAAG ATCACAGCCA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075274](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075274)



Table 1. Demographic characteristics of the study population	
Age	Mean (SD)
Sex	Male
Marital status	Married
Education	High school or above
Occupation	White-collar
Income	High
Health status	Good
Family size	Small
Religion	Christian
Marital satisfaction	High
Parental involvement	High
Child's gender	Male
Child's age	Mean (SD)
Child's height	Mean (SD)
Child's weight	Mean (SD)
Child's BMI	Mean (SD)
Child's blood pressure	Mean (SD)
Child's cholesterol	Mean (SD)
Child's glucose	Mean (SD)
Child's hemoglobin A1c	Mean (SD)
Child's liver enzymes	Mean (SD)
Child's kidney function	Mean (SD)
Child's thyroid function	Mean (SD)
Child's vitamin D	Mean (SD)
Child's iron	Mean (SD)
Child's zinc	Mean (SD)
Child's calcium	Mean (SD)
Child's magnesium	Mean (SD)
Child's potassium	Mean (SD)
Child's sodium	Mean (SD)
Child's chloride	Mean (SD)
Child's phosphorus	Mean (SD)
Child's selenium	Mean (SD)
Child's copper	Mean (SD)
Child's manganese	Mean (SD)
Child's chromium	Mean (SD)
Child's cobalt	Mean (SD)
Child's nickel	Mean (SD)
Child's vanadium	Mean (SD)
Child's molybdenum	Mean (SD)
Child's boron	Mean (SD)
Child's silicon	Mean (SD)
Child's aluminum	Mean (SD)
Child's gallium	Mean (SD)
Child's arsenic	Mean (SD)
Child's selenium	Mean (SD)
Child's tellurium	Mean (SD)
Child's iodine	Mean (SD)
Child's bromine	Mean (SD)
Child's fluorine	Mean (SD)
Child's oxygen	Mean (SD)
Child's hydrogen	Mean (SD)
Child's carbon	Mean (SD)
Child's nitrogen	Mean (SD)
Child's phosphorus	Mean (SD)
Child's sulfur	Mean (SD)
Child's chlorine	Mean (SD)
Child's potassium	Mean (SD)
Child's sodium	Mean (SD)
Child's calcium	Mean (SD)
Child's magnesium	Mean (SD)
Child's zinc	Mean (SD)
Child's iron	Mean (SD)
Child's copper	Mean (SD)
Child's manganese	Mean (SD)
Child's chromium	Mean (SD)
Child's cobalt	Mean (SD)
Child's nickel	Mean (SD)
Child's vanadium	Mean (SD)
Child's molybdenum	Mean (SD)
Child's boron	Mean (SD)
Child's silicon	Mean (SD)
Child's aluminum	Mean (SD)
Child's gallium	Mean (SD)
Child's arsenic	Mean (SD)
Child's selenium	Mean (SD)
Child's tellurium	Mean (SD)
Child's iodine	Mean (SD)
Child's bromine	Mean (SD)
Child's fluorine	Mean (SD)
Child's oxygen	Mean (SD)
Child's hydrogen	Mean (SD)
Child's carbon	Mean (SD)
Child's nitrogen	Mean (SD)
Child's phosphorus	Mean (SD)
Child's sulfur	Mean (SD)
Child's chlorine	Mean (SD)
Child's potassium	Mean (SD)
Child's sodium	Mean (SD)
Child's calcium	Mean (SD)
Child's magnesium	Mean (SD)
Child's zinc	Mean (SD)
Child's iron	Mean (SD)
Child's copper	Mean (SD)
Child's manganese	Mean (SD)
Child's chromium	Mean (SD)
Child's cobalt	Mean (SD)
Child's nickel	Mean (SD)
Child's vanadium	Mean (SD)
Child's molybdenum	Mean (SD)
Child's boron	Mean (SD)
Child's silicon	Mean (SD)
Child's aluminum	Mean (SD)
Child's gallium	Mean (SD)
Child's arsenic	Mean (SD)
Child's selenium	Mean (SD)
Child's tellurium	Mean (SD)
Child's iodine	Mean (SD)
Child's bromine	Mean (SD)
Child's fluorine	Mean (SD)
Child's oxygen	Mean (SD)
Child's hydrogen	Mean (SD)
Child's carbon	Mean (SD)
Child's nitrogen	Mean (SD)
Child's phosphorus	Mean (SD)
Child's sulfur	Mean (SD)
Child's chlorine	Mean (SD)
Child's potassium	Mean (SD)
Child's sodium	Mean (SD)
Child's calcium	Mean (SD)
Child's magnesium	Mean (SD)
Child's zinc	Mean (SD)
Child's iron	Mean (SD)
Child's copper	Mean (SD)
Child's manganese	Mean (SD)
Child's chromium	Mean (SD)
Child's cobalt	Mean (SD)
Child's nickel	Mean (SD)
Child's vanadium	Mean (SD)
Child's molybdenum	Mean (SD)
Child's boron	Mean (SD)
Child's silicon	Mean (SD)
Child's aluminum	Mean (SD)
Child's gallium	Mean (SD)
Child's arsenic	Mean (SD)
Child's selenium	Mean (SD)
Child's tellurium	Mean (SD)
Child's iodine	Mean (SD)
Child's bromine	Mean (SD)
Child's fluorine	Mean (SD)
Child's oxygen	Mean (SD)
Child's hydrogen	Mean (SD)
Child's carbon	Mean (SD)
Child's nitrogen	Mean (SD)
Child's phosphorus	Mean (SD)
Child's sulfur	Mean (SD)
Child's chlorine	Mean (SD)
Child's potassium	Mean (SD)
Child's sodium	Mean (SD)
Child's calcium	Mean (SD)
Child's magnesium	Mean (SD)
Child's zinc	Mean (SD)
Child's iron	Mean (SD)
Child's copper	Mean (SD)
Child's manganese	Mean (SD)
Child's chromium	Mean (SD)
Child's cobalt	Mean (SD)
Child's nickel	Mean (SD)
Child's vanadium	Mean (SD)
Child's molybdenum	Mean (SD)
Child	

BackwardPrimer : AGTGATTGCC CGAAATCATG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075274](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075274)

# SNP Information for IMS-JST075276

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

## General Information

JSNP ID : IMS-JST075276  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	684479	6	2977011

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CTGCCCTAG GCTAGGAGAG CTGGCAATG CCTGGAGACC CAAAGGCCTC ATCCTCAGGG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075276](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075276)

12/17/2001

# Sequence

Observed : C/A  
3' Assay : GGCCAACTCT TCTGTTTAG TGATATACAG ACTATCTTTT ATTGTGATTT ATAGTCAAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 (Graphical View of this Entry)  
Chromosome : 6  
map  
Definition of the record : Homo sapiens chromosome 6 working draft sequence  
e segment.  
Position in Sequence : 183612 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_026300.1 20010416\_4  
Amplified region : 182827..184053 in NT\_026300  
size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

TGGGT"EEG007

BackwardPrimer : ACTGGACAGC TGGGAACCTG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075276](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075276)

TOGETHER

# SNP Information for IMS-JST075279

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST075279  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Keyword

search

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	684621	6	2976869

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CCTGTATTCA TAAACTTTCT TTTTCCTTTC CTTCCTCACT GCCCAGCTTT AGGTTCAYYC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075279](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075279)

12/17/2001

TTTGAAGGGA TGAATGTGAC

Observed : T/C  
 3' Assay : TGTAAGTGTG GCTGCTGTCA GAATAGGAAC CTCCTGCGC TTTGAAGGGA TGAATGTGAC  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 (Graphical View of this Entry)  
 Chromosome : 6  
 map  
 Definition of the record : Homo sapiens chromosome 6 working draft sequence  
 e segment.  
 Position in Sequence : 183470 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_026300.1\_20010416\_4  
 Amplified region : 182827..184053 in NT\_026300  
 size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075279](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075279)

12/17/2001

Forward Primer : CCGGGGCTT

BackwardPrimer : ACTGGACACG TGGGACCTG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075279](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075279)

FASTA SEQUENCE

# SNP Information for IMS-JST075280

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

## General Information

JSNP ID : IMS-JST075280  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	684674	6	2976816

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTCAATCTTG TAAGTGTTGC TGGTGTCAGA ATAGGRACCT CCCTGGGCTT TGAAGGGATG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075280](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075280)

12/17/2001



# FOXP1 "E3E00T"

Observed : A/G  
3' Assay : ATGTGACCTC TCCACATTC TCCGGTGCTG TGATGTACCT TAAACACAGC AAGGTACTTG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 (Graphical View of this Entry)  
Chromosome : 6  
map  
Definition of the record : Homo sapiens chromosome 6 working draft sequence  
e segment.  
Position in Sequence : 183417 ([View SNP position in this record](#))

## Method

[PCR Method](#)  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_026300.1\_20010416\_4  
Amplified region : 182827..184053 in NT\_026300  
size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

TCCTTCCCT

BackwardPrimer : ACTGGACAGC TGGGAACCTG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075280](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075280)

SECRET EEO3E00F

# SNP Information for IMS-JST075282

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075282  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Keyword



## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	687511	6	2973979

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

NT\_026300.1

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : ACCCATCAA TCAGAGAGAA GGAATCCACC TTCTTAGCT ATGGCAGGTA ATGATTCACT  
 Observed : A/G  
 3' Assay : TTGTGGAGTA AGACTTTTT TTTTGTGAGA TGGGATTTT TTGTATTGCC CAGGCTGGTC  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 ([Graphical View of this Entry](#))  
 Chromosome : 6  
 map  
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
 Position in Sequence : 180580 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_026300.1\_20010416\_6  
 Amplified region : 179255..180775 in NT\_026300  
 size : 1521  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075282](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075282)

12/17/2001

PCR Cycle

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TGTCAGGAAG CAGCAGTGAT  
BackwardPrimer : ACATTGCAG ATATCAGCTA C



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075282](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075282)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075284

## General Information

JSNP ID : IMS-JST075284  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	688132	6	2973358

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075284](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075284)

12/17/2001

NT\_026300.1

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : CTGGGCCAGA TAATCCTATG TTTTGGGGG TCATCCTGTG CACCTGTTT AGCACCTAGC  
 Observed : A/C  
 3' Assay : CCATCCCTGG CCTCTGCCCA CCAGATGCCA GTAGCACCCC TCCCCCACCG GCTGTGACAA  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 ([Graphical View of this Entry](#))  
 Chromosome : 6  
 map  
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
 Position in Sequence : 179959 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_026300.1\_20010416\_6  
 Amplified region : 179255..180775 in NT\_026300  
 size : 1521  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TGTCAGGAAG CAGCAGTCAT  
BackwardPrimer : ACATTGCAG ATATCAGCTA C



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075284](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075284)

12/17/2001



TOGETHER

# SNP Information for IMS-JST075286

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

## General Information

JSNP ID : IMS-JST075286  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
U07736.1	genomic	NQ02	CDS*1	Annotated	
U07732.1	genomic	NQ02	exon*1	Annotated	

## Allele Sequence

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075286](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075286)

12/17/2001

# T02307-CE3E007

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GTAGATGAAC TGAGCAGGCA GGGCTGCACC GTCACAGTGT CTGATTGTA TGCCATGAAC  
Observed : T/C  
3' Assay : TTGAGCCGAG GGCCACAGAC AAAGATATCA CTGGTGAGTC ATGGGATAAA TGCTCTATTT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : U07732.1 ([Graphical View of this Entry](#))  
Chromosome : 6  
map  
Definition of the record : Human quinone oxidoreductase2 (NQO2) gene, introns 2 and 3 and exon 3.  
Position in Sequence : 372 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : U07732.1.20000425\_1  
Amplified region : 21..552 in U07732\_1  
size : 532  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35

## PCR condition

Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TTGCAGTCAG CTGAGTCATG C  
BackwardPrimer : GTGATAATCC CAGTGCTATC TA



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075286](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075286)

12/17/2001

# SNP Information for IMS-JST075290

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075290  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Keyword

search

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	695442	6	2966048

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

TOP of 663600

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ACGCTGAGCT CTCTGCTCTG CTTCTCTCTGT CCCCTTTGGG TCGGCCGGCC ACGTGGAGCC  
Observed : C/T  
3' Assay : GCTTTCCTCC TCGCACCCAC TCCACTCCCA TAACCCGGTG GCTGGGTAGG CTAAGACCTG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_026300.1 (Graphical View of this Entry)  
Chromosome : 6  
map :  
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
Position in Sequence : 172649 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_026300.1\_20010416\_8  
Amplified region : 172424..173856 in NT\_026300  
size : 1433  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

# PCR "SCREEN"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TATCCACGTA GCCAATATCA C  
BackwardPrimer : GCTCTGATAT TAGTAGTGCA G



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075290](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075290)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## SNP Information for IMS-JST075291

### General Information

JSNP ID : IMS-JST075291  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

### Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	696193	6	2965297

### Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

NT\_026300.1

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TCCTTTTGAC TGGCTTGATC ACAGACTGCT GCTCAAAGC TGGTGTACG CACAGCTCCT  
Observed : C/T  
3' Assay : GTCCCTCCC TGCCGTGCCA GGGCCAGCAT CAGGGGCTGT CATCACTGGG GGATGCAGAG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_026300.1 (Graphical View of this Entry)  
Chromosome : 6  
map  
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
Position in Sequence : 171898 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_026300.1.20010416.9  
Amplified region : 171031..172143 in NT\_026300  
size : 1113  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes



PCR "E3E00"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CGGTAACACT GGATGTAATG T  
BackwardPrimer : TCATAGCTAC CACATGTGGC A



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075291](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075291)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## SNP Information for IMS-JST075292

### General Information

JSNP ID : IMS-JST075292  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

### Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	696494	6	2964996

### Gene Information

#### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	CDS*1	Annotated	

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AGCCTCAGTT TCTCTTTGGT GTTCCCGCCC ACAGTTCCCG CTGTACTGGT TCAGCGTGCC  
Observed : A/G  
3' Assay : GCCATCCTGA AGGCTGGAT GGATAGGGTG CTGTGCCAGG GCTTTGCCTT TGACATCCCA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT 026300.1 (Graphical View of this Entry)  
Chromosome : 6  
map :  
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
Position in Sequence : 171597 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT 026300.1.20010416.9  
Amplified region size : 171031..172143 in NT\_026300 : 1113  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycling Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CGGTAACACT GGATGTAATG T  
BackwardPrimer : TCATAGCTAC CACATGTGGC A



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## SNP Information for IMS-JST075294

### General Information

JSNP ID : IMS-JST075294  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

### Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	696602	6	2964888

### Gene Information

#### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075294](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075294)

12/17/2001

NT\_026300.1

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CTTTGACATC CCAGGATTCT ACGATTCCGG TTTCCTCCAG GTATGTGCTC TTGGATAAGG  
Observed : A/T  
3' Assay : TCACATATGGA TAGTTGGAGG GAGGGACAG AGGATGCGTC TTCTATCAAG TTATATTTCT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_026300.1 ([Graphical View of this Entry](#))  
Chromosome : 6  
map  
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
Position in Sequence : 171489 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_026300.1 20010416\_9  
Amplified region : 171031..172143 in NT\_026300  
size : 1113  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : CGGTAACACT GGATGTAATG T  
 BackwardPrimer : TCATAGCTAC CACATGTGGC A



[illegible]

BackwardPrimer : AGTGGAGAT TCACTGCTGT



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075551](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551)

12/17/2001



TOPCAT 6635007

## Screened Sequence

Accession No. : U52852.2 (Graphical View of this Entry)  
Chromosome : 16  
map : 16p12.1  
Definition of the record : Homo sapiens TS PST1 (STP1) gene, complete cds.  
Position in Sequence : 3666 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : U52852.2\_20010313\_1  
Amplified region size : 3498..4618 in U52852 : 1121

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes

ForwardPrimer : GACCTTCACA CACCCTGATA TCT  
BackwardPrimer : TGGGATCTCT GGCTCACCAC AAC



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075311](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075311)

12/17/2001

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075348

## General Information

JSNP ID : IMS-JST075348  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029462.1	51841	16	72320063

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_010441.3	genomic	LOC82562	CDS*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075348](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075348)

12/17/2001

NT\_010441.3 "CE386001"

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TGGGGACTGG AAGACCACCT TCACCGTGGC GCAGAATGAG CGCTTCGATG CGGACTATGC  
Observed : G/A  
3' Assay : GACAAGATGG CAGGCTGCAG CCTCAGCTTC CGCTCTGAGC TGTGAGAGGG GCTCCTGGAG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_010441.3 (Graphical View of this Entry)  
Chromosome : 16  
map :  
Definition of the record : Homo sapiens chromosome 16 working draft sequence segment.  
Position in Sequence : 25476 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_010441.3 20010416\_1  
Amplified region : 24795..25705 in NT\_010441  
size : 911  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

# PCR "43300"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GAGTCATGG ACCACAGCAI  
BackwardPrimer : ACTCGACGTC CTCACCATC



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075348](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075348)

12/17/2001

TEXT "663300"

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

# SNP Information for IMS-JST075350

## General Information

JSNP ID : IMS-JST075350  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	351246	4	68051248

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TTAGACTTAC TAGTTATTGA TACCTCTTTG GCATGAAGAA AACATTTAAA TAGTCATTTA  
 Observed : T/C  
 3' Assay : AGCAATGCAC AGGTATAATA AAACCTCCAA TTATTAAAGA GGGTATTATT ATCTCTCCTT  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 ([Graphical View of this Entry](#))  
 Chromosome : 4  
 map  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
 Position in Sequence : 1248731 ([View SNP position in this record](#))

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3.20010416\_2  
 Amplified region : 1248329..1249405 in NT\_006281  
 size : 1077  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : GCCTTCTAT TCAGAGATGG C  
 BackwardPrimer : CTGAGGTTTG GATTCTGTTC C



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075350](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075350)

12/17/2001

For "663600"

# SNP Information for IMS-JST075352

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075352  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	339744	4	68039746

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	



Top of the page

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TTTTGGAGGT CAGTGTATT TTGCTGAAA TGCTTCTTT GTACTTGACA TAAAAAATA  
 Observed : T/C  
 3' Assay : CTGATGTTT TATATCCATA AATAGCTAAT TTTACTTTT AGATTGTCC TCATATTSTT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
 Chromosome : 4  
 map :  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
 Position in Sequence : 1260233 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3.20010416.3  
 Amplified region size : 1260005..1261237 in NT\_006281  
 : 1233  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

# PCR "CONDITIONS"

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : GCTAGAAGTC CATTATCAGT C  
 BackwardPrimer : AGATTCCAT AATGTGGCAT G



SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

Search

SNP Information for IMS-JST075355

General Information

JSNP ID : IMS-JST075355  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	339588	4	68039590

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AATTGATTT ACTATTGATG CAGAAATATT TAATTGATG AATGTTTATG AAAATAGACT  
Observed : T/C  
3' Assay : TTATCTGGTT TTAGTGGCCT ATGGTTCCTG GTTTACTCAT GTTAAAAAACT GGTGGAAGAA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 1260389 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3.20010416.3  
Amplified region : 1260005..1261237 in NT\_006281  
size : 1233  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR program

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : GCTAGAAATC CATTATCAGT C  
BackwardPrimer : AGATTCCAT AATGTGGCAT G



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075355](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075355)

12/17/2001

## SNP Information



SNP Home

[Search](#)[Search by HOWDY](#)[BLAST SNP](#)[FTP Server](#)[Search Example](#)Keyword 

## General Information

JSNP ID : IMS-JST075358  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	335985	4	68035987

## Gene Information

## Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075358](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075358)

12/17/2001

NT\_006281.3

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GTCTAAATTT AACTTAGAAG AATATGGCAT TTACTGTTGA AATACATTAC TTCCATTTAA  
Observed : G/A  
3' Assay : TAGTCTGTTT ATTGTGGCTT ATACACATAA TATATGTCAA AAATGTGTTA ATAATAACAA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 ([Graphical View of this Entry](#))  
Chromosome : 4  
Map :  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 1263992 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3.20010416.4  
Amplified region : 1262944..1264128 in NT\_006281  
size : 1185  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

Experiment Details

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCTACTATC ATCATGTCTG	C
BackwardPrimer	:	TATTGAAAAC AGATCGTGGC	





TOP LEFT: 66336001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075359

## General Information

JSNP ID : IMS-JST075359  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	333437	4	68033439

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STIB2	intron*1	Annotated	

Top of the page

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTCAAAATGTC AGACTCTATT TAATTATAAA CCACCTTCC AGATGTAATAA AATTATTCAA  
Observed : A/T  
3' Assay : TTTTAAAGC CTGAAAAATT TAAAGGTAA TACAATTAA AGACTGTTTG AATTCATTCA  
Comment :  
Sample size : 96

Screened Sequence

Accession No. : NT\_006281.3 ([Graphical View of this Entry](#))  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 1266540 (View SNP position in this record)

Method

PCR Method  
Sequence Method

PCR Profile

Screening region ID : NT\_006281.3.20010416.5  
Amplified region : 1266274..1267183 in NT\_006281  
size : 910  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "EFFECT"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CACAGTTTTC CTGTGCTGAT G  
BackwardPrimer : TGGACCATGG TACTAGGGAG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075368

## General Information

JSNP ID : IMS-JST075368  
dbSNP ID (rs#) :  
dbSNP ID (ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	839825	2	105891956

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005224.2	genomic	SULT1C1	intron*1	Annotated	

1023481

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TACATGAGAC AGCCTGCTGC AGGCACATGG GGTCACTC TGGCTGGCAG GAAGGTGAGG  
 Observed : G/C  
 3' Assay : AGTCCTCTCT TCTCTGGTCC TGGCTGACTC TGGCTCAGCA GGACTTCACT TGACCAATTCT  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_005224.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 1023481 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_005224.2.20010209\_4  
 Amplified region : 1022386..1023623 in NT\_005224  
 size : 1238  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR "EFFECT"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TGAGACAGTA GAAATCATGA C  
BackwardPrimer : CTGCCTGATT CATCTGTTA C



# SNP Information for IMS-JST075370

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075370  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Keyword

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	840639	2	105892770

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005224.2	genomic	SULT1C1	intron*1	Annotated	

102224.2

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : AAAAAGCTA AAGCTCTCCC CAAGGAGGC CAGCGCGGT GGCTACGCC TGTAAATCCCA  
 Observed : G/C  
 3' Assay : CACTTTGGGA GGCGAGGCG SGTGCATCAC AAGTCAGGA GATCGAGAGC ACGGTGAAAC  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_005224.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 1022667 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_005224.2.20010209\_5  
 Amplified region : 1021644..1022832 in NT\_005224  
 size : 1189  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075370](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075370)

12/17/2001



PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TGAGTGCAGT AAGCGTAGCT  
BackwardPrimer : AGGTCAAGGC AGAGTGGTTC



## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075374

## General Information

JSNP ID : IMS-JST075374  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	918099	2	105970230

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005224.2	genomic	LOC65351	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075374](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075374)

12/17/2001

NT\_005224.2 "E433E00T"

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ACTTTCCAG GAGAGAGTGA AACACAGTTAA GAGCAAAAGG GTAGACTTGT TTATTTATTC  
Observed : A/C  
3' Assay : TTCCCAATCT AGGCCCTTAT TGTAGATCTT GTAAAAAGCT GCCTTGAGTG TGTGAGCTAG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : [NT\\_005224.2](#) ([Graphical View of this Entry](#))  
Chromosome : 2  
Map :  
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
Position in Sequence : 948390 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_005224.2\_20010209\_7  
Amplified region : 947576..948773 in NT\_005224  
size : 1198  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

Sequence

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CGACAGACAC CTGTGACATC  
BackwardPrimer : CTTAAACCTC ATTAATGCCA TGA



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075380

## General Information

JSNP ID : IMS-JST075380  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	924463	2	105976594

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AGCAGACAA CCTATGAGGT TATCAGTATA AAATTCCTT CTTTGTGTTT ACTTTGTTTT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075380](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075380)

12/17/2001

TGAGTTCCTT

Observed : T/C  
3' Assay : ACTTGGTACA AAAGTGTGT GCCACCATAC GAAGACTCCA GGCAGATGAT GTTCCCTAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_005224.2 (Graphical View of this Entry)  
Chromosome : 2  
map  
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
Position in Sequence : 1383482 ([View SNP position in this record](#))

## Method

[PCR Method](#)  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_005224.2 20010209\_9  
Amplified region : 1383149..1384258 in NT\_005224  
size : 1110

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCTTGATCT CAACAGGTGC	T

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075380](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075380)

12/17/2001

THE UNIVERSITY OF CHICAGO

Top "Sequence"

BackwardPrimer : ACAATGACAT ACAGTGCTA G



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075380](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075380)

12/17/2001



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075427

## General Information

JSNP ID : IMS-JST075427  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	1359216	19	64551367

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011190.3	genomic	SULT2A1	intron*1	Annotated	

Top of Page

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GTGATCGGCC CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCATGAGC CACGGCGCCC  
Observed : G/A  
3' Assay : GCCAATTTAT CAGCTTTAAT TGCTCATCGC CCAGAACACT TCTCCCGTGG CCTCAGCAGG  
Comment : repeat sequence (SNP is present in repeat sequence)  
Sample size : 96

## Screened Sequence

Accession No. : NT\_011190.3 (Graphical View of this Entry)  
Chromosome : 19  
map :  
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
Position in Sequence : 1117678 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_011190.3 20010417\_3  
Amplified region : 1117026..1117896 in NT\_011190  
size : 871  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075427](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075427)

12/17/2001

# Sequence

Annealing : 62.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CTGGGATTAC AGCGTGAAC  
BackwardPrimer : TAGTTACCT GCTCACTGTC T



# SNP Information for IMS-JST075428

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

## General Information

JSNP ID : IMS-JST075428  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	1356250	19	64554333

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CCTGAAACCT TAAATATCAA ACCTCTGCAT CTCTGATCCC TTCCTTGTTA AAAGTTACCA

# Sequence

Observed : G/C  
 3' Assay : GGTGGCCAG GCRGGTGGT TCATGCCCTCT AATCCCAGCA CTATGGGAGG CCGAGACGGG  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011190.3 (Graphical View of this Entry)  
 Chromosome : 19  
 map  
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
 Position in Sequence : 1120644 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_011190.3.20010417\_4  
 Amplified region size : 1120220..1121152 in NT\_011190 : 933

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGGAATAAC TATGTGACCA	G

BackwardPrimer : TGACTCAACT CACTGCAAC



TOP SECRET 4686007

# SNP Information for IMS-JST075429

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075429  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Keyword

search

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	1356237	19	64554346

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ATATCAAAAC TCATCATCTC TGATCCCTTC CTTGTTAAAA GTTACCASGG TTGGCCAGGC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075429](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075429)

12/17/2001

# Footnote

Observed : A/G  
 3' Assay : CCGTGGTTCA TGCCTGTAAT CCGAGCACTA TGGGAGGCCG AGACGGCGG ATCACCAGGT  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011190.3 (Graphical View of this Entry)  
 Chromosome : 19  
 map  
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
 Position in Sequence : 1120657 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_011190.3.20010417\_4  
 Amplified region : 1120220..1121152 in NT\_011190  
 size : 933

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGTGAATAAC TATGTACCA	G



Age	Sex
18-24	Male
25-34	Male
35-44	Male
45-54	Male
55-64	Male
65-74	Male
75-84	Male
85+	Male
18-24	Female
25-34	Female
35-44	Female
45-54	Female
55-64	Female
65-74	Female
75-84	Female
85+	Female
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both
65-74	Both
75-84	Both
85+	Both
18-24	Both
25-34	Both
35-44	Both
45-54	Both
55-64	Both

BackwardPrimer : TGACTCAACT CACTGCAAC



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075429](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075429)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075435  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	453137	19	65457446

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011190.3	genomic	SULT2B1	intron*1	Annotated	

NT\_011190.3 "CEBCEOOT"

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AGGCAGCCCC AGGTTAGGAC CCAGACATGC GGATCCCAGG TTCCACGCTC CTCCTTGGC  
Observed : C/T  
3' Assay : GAGTGCCTC CCTCGCTGA CCCCTCTCCC CTGCTGCAG GACTTACAGG GTCCTGTTGA  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_011190.3 ([Graphical View of this Entry](#))  
Chromosome : 19  
map  
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
Position in Sequence : 82713 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_011190.3.20010417.8  
Amplified region : 82273..82895 in NT\_011190  
size : 623  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : ACCTATTCCC TCCCACTAG  
BackwardPrimer : GTCGTTGGGA GTTCTCTGGA



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075435](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075435)

12/17/2001

# SNP Information for IMS-JST075436

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075436  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	451136	19	65459447

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011190.3	genomic	SUL.T2B1	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075436](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075436)

12/17/2001

NT\_011190.3

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GCGCCAATCA GCAATTGTT TGCAAGCCCT GAGCACAGAG CCTGCAAG GGGTCCCTT  
Observed : C/T  
3' Assay : CATGTCCAAG CAGTAATGGC TGCAGCATGG AGORTTGTGG GGCATTGAG ACAGGAGGCC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_011190.3 ([Graphical View of this Entry](#))  
Chromosome : 19  
map :  
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.  
Position in Sequence : 80712 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_011190.3\_20010417\_9  
Amplified region : 79864..80803 in NT\_011190  
size : 940  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075436](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075436)

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : AGGCTTGGAG GGTTCCTGAG  
BackwardPrimer : CTGCAGCACC TTGCCCTCTG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075486

## General Information

JSNP ID : IMS-JST075486  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	10166541	22	27418329

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GAGGAGACTG AGGCTTAGGG AGGGTGAGGT TCATAGCTTC ATGCCTAAGT TTACAGTAGC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075486](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075486)

12/17/2001



TTAGTCTCCTACACAGGATC

Observed : T/C  
 3' Assay : AGGCAGGAAA GGCACAACCA GCCTTGGACC COTCAGTGG CTGGACGGG AGGCAGGAC  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_011520.5 (Graphical View of this Entry)  
 Chromosome : 22  
 map  
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
 Position in Sequence : 10168640 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_011520.5.20010417\_12  
 Amplified region : 10168482..10169592 in NT\_011520  
 size : 1111

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TAGGTCTCCT ACACAGGATC	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075486](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075486)

12/17/2001

BackwardPrimer : GGACAGGAAG CTCTATCCTG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075486](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075486)

12/17/2001

TOGETHER WE CAN SAVE LIVES

# SNP Information for IMS-JST075493

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075493  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	10160723	22	27412511

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	CST	CDS*1	Annotated	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP\\_ID=IMS-JST075493](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-JST075493)

[illegible]

## Allele Sequence

Variation Type	:	SNP
Flanking Sequence	:	Information
5' Assay	:	GGAGCGCGCA
Observed	:	C/T
3' Assay	:	GGGAGTGCCA
Comment	:	GGCGCGCGC AACATCGTGT TCTTGAAGAC GCACAAGACG
Sample size	:	96

## Screened Sequence

Accession No.	:	NT_011520.5	(Graphical View of this Entry)
Chromosome	:	22	
map	:		
Definition of the record	:	Homo sapiens chromosome 22 working draft sequence segment.	
Position in Sequence	:	10162822	(View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID	:	NT_011520.5_20010417_16			
Amplified region	:	10162183..10163173	in	NT_011520	
size	:	991			
Pre-Denature	:	94.0	degrees	C	for
Denaturation	:	94.0	degrees	C	for
					2.00 minutes
					0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075493](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075493)

12/17/2001

PCR program

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TGGTACATGC AACACAGTGG  
BackwardPrimer : GTTGAGCTTG AACTAGAGCA C



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075493](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075493)

12/17/2001

## SNP Information



## Search

BLAST SNP

## Search Example

#### Keyword

search

## NEW Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	402804	4	68102806

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTTTATTAT TAATATCAAT ACATTAGATT TAGATATATA AATATACAA TGAAAAATTAT

12/17/2001

# Sequence

Observed : G/A  
 3' Assay : TATTACAAAG CTCTTAAAAA TAAAAATATAC AAAGACCAAA GTCTTGATTG ATACTTAGT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
 Chromosome : 4  
 map  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
 Position in Sequence : 1197173 ([View SNP position in this record](#))

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3.20010416.8  
 Amplified region : 1196916..1197777 in NT\_006281  
 size : 862

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGTCTGATTG AGGTCCTTG	

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075563](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075563)

BackwardPrimer : ACCTCCTTCT ACCCTGCTTG





# SNP Information for IMS-JST075565

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST075565  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403390	4	68103392

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GAACATGTA CAAAAGTCAC TTTTGCTCA TACAGTAA TCTAGAAAG TAGGACTAT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075565](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075565) 12/17/2001

PCR "SCREEN"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CGGTCTCTGCC TCCTTTAATG  
BackwardPrimer : GACAACCAGA TGATGAGGTG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075539](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075539)



# SNP Information for IMS-JST075566

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

BLAST SNP

FTP Server

[Search Example](#)

## General Information

JSNP ID : IMS-JST075566  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403406	4	68103408

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TCACCTTTGC CTCATACAGG TAAATCTAAG AAAGTAGGGA CTATGAGAAC CCCATATGTAT

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075566](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075566)

TTGAGGTTTGGGAGGCT

Observed : C/T  
 3' Assay : TATATCCACC ATAGTATTCT AGCACTGACT ACAGGGGCTA GGAAGGGT AGGCATTTCAC  
 Comment : repeat sequence (SNP is present in repeat sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
 Chromosome : 4  
 map  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence  
 e segment.  
 Position in Sequence : 1196571 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

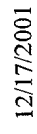
Screening region ID : NT\_006281.3.20010416\_9  
 Amplified region : 1196173..1197306 in NT\_006281  
 size : 1134

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GATCTGCCTT GGTAATTGAA G	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075566](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075566)

12/17/2001

BackwardPrimer : GAGGCAAAGT AGGTGGCATG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075566](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075566)

**SNP Information for IMS-JST075567**



## General Information

JSNP ID : IMS-JST075567

dbSNP ID(rs#) :

dbSNP ID (ss#)

HGBASE ID : :

Organism : Homo sapiens

Molecular type : Genomic

Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN

Citation : J Hum Genet. 2001;46(4):225-40

Release Date : 2001/06/11

Last Update : 2001/06/11

**Keyword**

Journal Pre-proof

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403507	4	68103509

## Gene Information

## Allele Sequence

Flanking Sequence Information

5' Assay : GGAAAAGGGT AGGCATTCAC ATAGGAGTA TTTGCTGGAT AAAAGGCAGG TTGGAAGATG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075567](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075567)

NT\_006281.3

Observed : C/A  
 3' Assay : AGGAGGGGAG TATGAGAGAA GAAAGGAGAA AAGAGAGGAA GGAGAGCGG AAGGAAAAAC  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
 Chromosome : 4  
 map  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence  
 e segment.  
 Position in Sequence : 1196470 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3 20010416\_9  
 Amplified region : 1196173...1197306 in NT\_006281  
 size : 1134

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GATCTGCCTT GGTATTGAA G	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075567

## General Information

JSNP ID : IMS-JST075567  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403507	4	68103509

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GGAAGAAGGT AGGCATTAC ATAGGAGTA TTGCTGGAT AAAAGGCAGG TTGGAAGATG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075567](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075567)

12/17/2001

TTGGGTTTGGGGGGT

Observed : C/A  
 3' Assay : AGGAGGGGAG TATGCAGAAA GAAAGGAAGA AAGAGAGGAA GGAGAGCGGG AAGGAAAAAC  
 Comment : repeat sequence (repeat sequence exists in flanking sequence)  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
 Chromosome : 4  
 map :  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence  
 e segment.  
 Position in Sequence : 1196470 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3 20010416.9  
 Amplified region : 1196173..1197306 in NT\_006281  
 size : 1134

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GATCTGCCTT GGTATTGAA G	

Forward Primer : CCGGCGGCT

BackwardPrimer : GAGGCAAAGT AGGTGGCATG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075567](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075567)

12/17/2001

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

# SNP Information for IMS-JST075568

## General Information

JSNP ID : IMS-JST075568  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	404450	4	68104452

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : AATAGATTGT CATGGGATCA GGAGATGAAT TAGGAAATGA TAACCATCTT GCTTAACCTT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075568](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075568)

12/17/2001

Observed : A/G  
3' Assay : TCATTTTATAG CCAAGTCATT CAATGGGAGT ATCCACTACC TTATTCATCG AATGGGGAAA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence  
e segment.  
Position in Sequence : 1195527 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_006281.3.20010416.10  
Amplified region : 1194357..1195580 in NT\_006281  
size : 1224

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extention	:	72.0 degrees C for	7.00 minutes

ForwardPrimer : TGTCATGGGA TCAGGAGATG

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075568](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075568)

12/17/2001

TTGAGTGGGAGG

BackwardPrimer : AATGGTGGTC ATACGCTGTA



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075568](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075568)

12/17/2001

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

# SNP Information for IMS-JST075569

## General Information

JSNP ID : IMS-JST075569  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	404663	4	68104665

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TCCTTTAAAT ACATTCACCA AGCATTGGT TTATTTAAA AAATGATACA TATTCAGGAA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075569](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075569)

12/17/2001

Observed : A/G  
3' Assay : TCAAAATCT CTGACTTAGA TACCYGGCAA TAAATATCAA ATGTAATGAT CTTATTGTT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence  
segment.  
Position in Sequence : 1195314 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3 20010416\_10  
Amplified region : 1194357..1195580 in NT\_006281  
size : 1224

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TGTCATGGGA TCAGGAGATG	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075569](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075569)

12/17/2001



Variable	Unit
Age	Years
Gender	Male/Female
Marital status	Married/Single/Divorced
Education	Years of schooling
Occupation	Various categories
Income	Monthly income
Health status	Good/Poor
Religious affiliation	Various religions
Political affiliation	Various parties
Urban/rural	Urban/Rural
Region	Various regions
Time of day	Day/Night
Season	Spring/Summer/Autumn/Winter
Weather	Sunny/Cloudy/Rainy
Temperature	Degrees Celsius
Humidity	Percentage
Wind speed	Meters per second
Pressure	Hectopascals
Altitude	Meters
Latitude	Degrees
Longitude	Degrees
Population density	Persons per square kilometer
Urbanization	Percentage of urban population
Infrastructure	Various indicators
Healthcare access	Distance to nearest health facility
Education access	Distance to nearest school
Employment	Unemployment rate
Income inequality	Gini coefficient
Corruption	Corruption index
Trust	Trust index
Cooperation	Cooperation index
Participation	Participation index
Empowerment	Empowerment index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index
Transformability	Transformability index
Reconfigurability	Reconfigurability index
Resilience	Resilience index
Adaptability	Adaptability index

BackwardPrimer : AATGGTGGTC ATACGCTGTA



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IJT075569](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IJT075569)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075577

## General Information

JSNP ID : IMS-JST075577  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	410462	4	68110464

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

Top of the page

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TACAAAAGTC TGAAGTAACA TAGAAGTAAT GATCAATGAC TACATGAAC TAGAGAAATCA  
 Observed : A/G  
 3' Assay : GTAGATCACA CACACCAACA ATAAATTAC ACAGATGAT AAAAGAATTT GAATGGAGAG  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
 Chromosome : 4  
 map :  
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
 Position in Sequence : 1189515 (View SNP position in this record)

## Method

PCR Method  
 Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3.20010416\_13  
 Amplified region : 1189368..1190522 in NT\_006281  
 size : 1155  
 Pre-Denature : 94.0 degrees C for 2.00 minutes  
 Denaturation : 94.0 degrees C for 0.50 minutes

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : AGCTGACGGT TTACACTGTC  
BackwardPrimer : TATACCTCTC CTATCTGATG C



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075577](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075577)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075579

## General Information

JSNP ID : IMS-JST075579  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	414009	4	68114011

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : AAGAAAGGGT GCAGNATAGT CTAGTATCTA AAGAGGCCA TTCTGATCAT GTAGTAACAA  
Observed : T/C  
3' Assay : TATAAGAAA ATAATAATGT GTTTTCATAT CCACAGATGA TAATATTGAC TCAAGACAAA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 ([Graphical View of this Entry](#))  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 1185968 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3 20010416\_14  
Amplified region : 1185499..1186704 in NT\_006281  
size : 1206  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycling

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TCTAATGGTG GCTGGTCATC  
BackwardPrimer : CCCTTAGTGT CATCTCACT C



FOR THE "CECCEOT"

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075580

General Information

JSNP ID : IMS-JST075580  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	414325	4	68114327

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	



Top of Page

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CTAATGGAGT CAAAGAACAG AGGAGGCATA CAATGACTTC AGGCAAAGCA GAACCTTTTG  
Observed : A/C  
3' Assay : CTCACACAAC ATTATATTAT TTGTCAGCT TTATATTITA TGAACACATT TTAATATGAG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
Chromosome : 4  
map :  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 1185652 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006281.3.20010416.14  
Amplified region : 1185499..1186704 in NT\_006281  
size : 1206  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

Position 663600

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : TCTAATGGTG GCTGGTCATC  
BackwardPrimer : CCTTAGTGT CATTCTCACT C



SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST075584

General Information

JSNP ID : IMS-JST075584  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	419468	4	68119470

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

Top of the page

# Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTGATTATA TGTTCCTTT TTCAAATTC TACATATAA TGTACAGAG GACTTAAAC  
Observed : A/G  
3' Assay : GTTGCTTGC TTGCAACGG TGAATTGCTG CTGTACCCTC AGAACCTATC TGATTTTTT  
Comment :  
Sample size : 96

# Screened Sequence

Accession No. : NT\_006281.3 (Graphical View of this Entry)  
Chromosome : 4  
map :  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 1180509 (View SNP position in this record)

# Method

PCR Method  
Sequence Method

# PCR Profile

Screening region ID : NT\_006281.3.20010416.15  
Amplified region : 1180366..1181496 in NT\_006281  
size : 1131  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

# PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CATCAGAGGA GCTTGTTGAC  
BackwardPrimer : GTTCACTTGC CCTCTTGCTC



TOP LEFT: 44336001

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105158

## General Information

JSNP ID : IMS-JST105158  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HCBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007402.5	1061191	6	56512411

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TCCTTTCTCG GACAGTCATT TTATTCTGA TAAAGCGTT CTTTCTTATG CATTGCAAA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105158](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105158)

12/17/2001

[illegible]

BackwardPrimer : AGTGGAGAT TCACTGCTGT



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075551](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551)

12/17/2001

TGGGTTTGGGGGTT

BackwardPrimer : CCTGGGAGAG ATTAGCACTA



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105158](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105158)

12/17/2001



# SNP Information for IMS-JST105159

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST105159  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007402.5	857593	6	56716009

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : GTGCGTATT TTTTAAAC CCTTCTGCG GAGTCTGAAT GCATTGGTGG AAGCTGGGCT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105159](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105159)

12/17/2001

Observed	:	C/T
3' Assay	:	GGATCGTCCC CGGCCTGGC TGGCTGCCG CTACGCCCT GCATGGCTG AGCGGGGAAG
Comment	:	
Sample size	:	96

```

Accession No.      : NT_007343.3 (Graphical View of this Entry)
Chromosome        : 6
map              :
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 2411915 (View SNP position in this record)

```

PCR Method	Sequence Method
------------	-----------------

Screening region ID	:	NT_007343.3.20010416.7	
Amplified region	:	2411339..2412239 in NT_007343	
size	:	901	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TCGTACTAGA	GCTTCAGCAG

12/17/2001

TGGGTT " GGGGGT

BackwardPrimer : GGAAATCGC ACAGCCACTG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105159](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105159)

12/17/2001

TOP LEFT "66332007"

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

# SNP Information for IMS-JST105163

## General Information

JSNP ID : IMS-JST105163  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007402.5	869160	6	56704442

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_007343.3	genomic	GSTA4	intron*1	Annotated	

Top " E68600T

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ATATTTGACC TGGAAATTGTG TTGGGAGTCC CTCTGACACA CACACTTGTG CACATGCAGA  
Observed : C/T  
3' Assay : ACCCATGGGC ATCCAAGAGT TGACTGTGAA GGGGATCTCC CCTTTGCTAC YACTGCTTCT  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_007343.3 ([Graphical View of this Entry](#))  
Chromosome : 6  
map  
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.  
Position in Sequence : 2423482 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_007343.3.20010416.11  
Amplified region : 2423025..2424109 in NT\_007343  
size : 1085  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Condition

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : GACCATCTTT ATGGAAGTAG AT  
BackwardPrimer : GCAGTATCTG AGAAGAGGTG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105069

## General Information

JSNP ID : IMS-JST105069  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004966.5	3635060	1	114067278

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_004966.3	genomic	GSTM4	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105069](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105069)

12/17/2001

NT\_004966.3

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GTGACAGTAT TCTTATTCA GTCCTGCCAT GAGCAGGCAC AGTGAGTGCC CGGTCTCCTC  
Observed : T/C  
3' Assay : CTGCTCTTGC TTATGGGAG GGGATGCTGG GGAGCCTGGT GGCCCAACTG AGCTTCGGCG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_004966.3 ([Graphical View of this Entry](#))  
Chromosome : 1  
map  
Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.  
Position in Sequence : 493791 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_004966.3.20010416.3  
Amplified region : 492835..493989 in NT\_004966  
size : 1155  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes



PCR Program

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : GTGCAACGTG TCTCTGACTG  
BackwardPrimer : AGGAGCTCA GGGAAAGTAG



Top of the page

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST075522

General Information

JSNP ID : IMS-JST075522  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2733857	2	98509980

Gene Information

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GGGAAACCCGC GGGTTTGTGC CTGGCGAGCC ACATCCCGGT GTGTTTGGC GACTTGAAGA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075522](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075522)

12/17/2001

# Sequence

Observed : C/T  
 3' Assay : CTCCTAGTT GCGGGAGTA GCGGGAAGAG CCTTCCTCGC GTTAATTATG CAATAAGAAAG  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_022171.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map :  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence  
 Position in Sequence : 526155 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_022171.2 20010209\_1  
 Amplified region : 525548..526488 in NT\_022171  
 size : 941

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TTTTCCTGGAT GGAGGCCAG C	

12/17/2001

CTCTGACAG CGAAGATCAG

BackwardPrimer : CTCTGACAG CGAAGATCAG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075522](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075522)

12/17/2001

**SNP Information for IMS-JST075524**

## SNP Information



SNP Home

## Search

Search by HOWDY

BLAST SNP

FTP Server

## Search Example

JSNP ID	: IMS-JST075524
dbSNP ID(rs#)	:
dbSNP ID(ss#)	:
HGBASE ID	:
Organism	: Homo sapiens
Molecular type	: Genomic
Laboratory	: Laboratory for
Citation	: J Hum Genet. 2001
Release Date	: 2001/06/11
Last Update	: 2001/06/11

### **Keyword**

search

## NEW Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2732905	2	98509028

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ATGAAATATG GAGTGTTC C AAGAAAGGA AAGAACTGAAC AAGAATTGT AAACATCACA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075524](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075524)

12/17/2001

TTGCTTTCAT CCTGGCTGA G

Observed : G/A  
3' Assay : GCAACTTGCA GTTATATTCG GATCATTTTT CAGTGTTTTGA GGAGTTTCATA CAATAAAAAAG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_022171.2 (Graphical View of this Entry)  
Chromosome : 2  
map  
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
Position in Sequence : 527107 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_022171.2.20010209.2  
Amplified region size : 526278..527279 in NT\_022171 : 1002  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : CTTCCTTTCAT CCTGGCTGA G

--- SNP INFORMATION ---  
TGGGTTTGGGCGGTT

BackwardPrimer : CATCCAGGTT ATCCAGAAAGT G



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075524](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075524)

## SNP Information



SNP Home

SearchSearch by HOWDY

BLAST SNP

FTP Server

### Search Example

## Keyword

\_\_\_\_\_

search

**SNP Information for IMS-JST075527**

## General Information

JSNP ID	:	IMS-JST075527
dbSNP ID(rs#)	:	
dbSNP ID(ss#)	:	
HGBASE ID	:	
Organism	:	Homo sapiens
Molecular type	:	Genomic
Laboratory	:	Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation	:	<u>J Hum Genet. 2001;46(4):225-40</u>
Release Date	:	2001/06/11
Last Update	:	2001/06/11

## NEW Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2731721	2	98507844

## Gene Information

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TCTTGTRACT TTTAATAATG CTTTTTTTTT TTTAATTTTC CTATCCACTG ACAAGAGGAA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075527](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075527)



NT\_022171.2

Observed : C/A  
 3' Assay : CAAGAACCTC AGTTCAGGGG AAACACAGCA AGGAATGTG AGCCCCAGGC TGCAGAAGGT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_022171.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 528291 ([View SNP position in this record](#))

## Method

[PCR Method](#)  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_022171.2.20010209\_3  
 Amplified region : 527752..528439 in NT\_022171  
 size : 688

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCCAGTCAGC TTGGGCTTTA	T

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075527](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075527)

12/17/2001

# Sequence

BackwardPrimer : TTTACAATCT GCACAGGCAA G



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075527](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075527)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

# SNP Information for IMS-JST075539

## General Information

JSNP ID : IMS-JST075539  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2662111	2	98438234

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022171.2	genomic	HNK-1ST	intron*1	Annotated	

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : GGGGAGGACA GCAAGGAGGA GTCACAAGAG GGCTGGTTTG ACCTGAAGGG ACTGGTGGCC  
Observed : G/T  
3' Assay : TCCAGACAGG CCTGTTTTTG TTGTTTCCTG TTAGTGTTGT GCCTTACAAG TTAGTGGGGC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_022171.2 ([Graphical View of this Entry](#))  
Chromosome : 2  
map  
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
Position in Sequence : 541579 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_022171.2.20010209.9  
Amplified region : 541167..542399 in NT\_022171  
size : 1233  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "SCREEN"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : CGTCTCTGCC TCCTTTAATG  
BackwardPrimer : GACAACCAGA TGATGAGGTG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075539](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075539)

FOREF "E63E00T

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST075548

General Information

JSNP ID : IMS-JST075548  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2657464	2	98433587

Gene Information

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : ACCAGGTGAA GATCTGAGCC CAGAAATGAC CCTTCCTCCA CCACACCCCT CCTTTGAGGA

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075548](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075548)

12/17/2001

# Sequence

Observed : C/T  
 3' Assay : GCCCGGGGTC TCCACAGGC CTGTGAGTTG CCTCGGCATA TGACGCAGAA CCCCCACTGT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_022171.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence  
 e segment.  
 Position in Sequence : 546226 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_022171.2 20010209\_13  
 Amplified region : 545838..547022 in NT\_022171  
 size : 1185

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGACGTATG TAGAGCTCTG	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075548](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075548)

12/17/2001

TTCTTTT

BackwardPrimer : AGTGGAGAT TCACTGCTGT



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075548](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075548)

12/17/2001



# SNP Information for IMS-JST075551

## SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST075551  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2657102	2	98433225

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TGCAGGAACA GCACCCAGGA CTCTGAGGAG GGACAGAGAA GCAAGGGGGC TGCTGAAATC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075551](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551)

12/17/2001

TCCTTCCCT

BackwardPrimer : AGGTGGAGAT TCAC TGCTGT



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075548](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075548)

TOP LEFT: 44336007

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

# SNP Information for IMS-JST075551

## General Information

JSNP ID : IMS-JST075551  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2657102	2	98433225

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TGCAGGAACA GCACCCAGGA CTCTGAGGAG GGACAGAGAA GCAAGGGGGC TGCTGAAATC

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075551](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551)

12/17/2001

TTGAGTTTGGGGGGT

Observed : G/C  
3' Assay : CAGAGACTTT TGCAGCATCA GATCTGAGGA GTAAACGGC ACCTCTGGCC TTCATCTTGG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_022171.2 (Graphical View of this Entry)  
Chromosome : 2  
map  
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
Position in Sequence : 546588 ([View SNP position in this record](#))

### Method

[PCR Method](#)  
[Sequence Method](#)

### PCR Profile

Screening region ID : NT\_022171.2.20010209\_13  
Amplified region size : 545838..547022 in NT\_022171 : 1185

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGACGATG TAGAGCTCTG	

[illegible]

BackwardPrimer : AGTGGAGAT TCACTGCTGT



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075551](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST075553

## General Information

JSNP ID : IMS-JST075553  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HGBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(4):225-40  
 Release Date : 2001/06/11  
 Last Update : 2001/06/11

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2656813	2	98432936

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TTCATTTCAGC ACAAGACATA CGATTTTAGA AGGTGAGGGG AGGGGAGGCT TTTTCTACCT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075553](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075553)

12/17/2001

# FOR THE "GENE" PROJECT

Observed : G/A  
 3' Assay : AGAAGGGGAG TGTCCTTTGAG GGCCTTAAAA GGACCATGGC CCAGGAATGG GGGCGCTGGT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_022171.2 (Graphical View of this Entry)  
 Chromosome : 2  
 map :  
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.  
 Position in Sequence : 546877 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_022171.2 20010209\_13  
 Amplified region size : 545838..547022 in NT\_022171 : 1185

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGACGTATG TAGAGCTCTG	

# SNP Detail

BackwardPrimer : AGGTGGAGAT TCACTGCTGT



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST075553](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075553)

12/17/2001



# SNP Information for IMS-JST105117

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105117  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008541.5	4035179	9	83945560
NT_008541.5	5158989	9	82821750

## Gene Information

## Allele Sequence

Variation Type : SNP

# Sequence

Flanking Sequence Information  
5' Assay : CTGCGCCTCC ATGGCTCTGC AGATCCTCTG GGAAGCGGCC CGCCACCTGT GACCAGCAGC  
Observed : T/G  
3' Assay : GATGCCCTCT TGGCCACCAG ACCATGGGCC AAGAGCCGCC GTGGCTATAC CTGGGGACTT  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_008541.3 (Graphical View of this Entry)  
Chromosome : 9  
map  
Definition of the record : Homo sapiens chromosome 9 working draft sequence segment.  
Position in Sequence : 589170 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_008541.3 20010416\_2  
Amplified region : 588076..589240 in NT\_008541  
size : 1165  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes  
Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

--- SNP INFORMATION ---

Forward Primer : AACCAGCAGA AGTAGGTGAG

Backward Primer : AAGGAACATC AGTCCCCAG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105117](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105117)

TEXT REFORMAT

# SNP Information for IMS-JST105119

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105119  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	495606	4	138937022

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105119](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105119)

12/17/2001

NT\_006124.3

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : TTGCAGGTAG CTCTGGGTCC TCAGAGCACA GTCCGCTCAG GGTCACCCAT GCCGCCGTGCT  
Observed : A/C  
3' Assay : CCCTCCTTCC CAGGGCAAG CAGAGACYGA GAACATTCCA GAGATTAGTT CTCCCAACTG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_006124.3 ([Graphical View of this Entry](#))  
Chromosome : 4  
map :  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 495592 (View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_006124.3.20010416\_1  
Amplified region : 495156..496414 in NT\_006124  
size : 1259  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105119](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105119)

12/17/2001

PCR "483600"

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCACAGTCTC TAGGTGACAG  
BackwardPrimer : CAAATGTGAC TCCCATGGAG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105119](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105119)

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST105120

General Information

JSNP ID : IMS-JST105120  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	495578	4	138937050

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

TOP SECRET 4436007

### Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CAGTCGCCTC AGGGTCACCC ATGCCGCCTG CTMCCCTCCT TCCAGGGGC AAGCAGAGAC  
Observed : T/C  
3' Assay : GAGAACATTC CAGAGATTAG TTCTCCCAAC TGGAACGCTG TGGGGCCTCA GAGCTCAGCG  
Comment :  
Sample size : 96

### Screened Sequence

Accession No. : NT\_006124.3 ([Graphical View of this Entry](#))  
Chromosome : 4  
map  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 495564 (View SNP position in this record)

### Method

PCR Method  
Sequence Method

### PCR Profile

Screening region ID : NT\_006124.3.20010416.1  
Amplified region : 495156..496414 in NT\_006124  
size : 1259  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes



PCR REACTION

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
  
ForwardPrimer : TCAGAGTCTC TAGTGACAG  
BackwardPrimer : CAAATGTGAC TCCCATGGAG



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105120](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105120)

TOGETHER" CEES&OOT

# SNP Information for IMS-JST105126

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

## General Information

JSNP ID : IMS-JST105126  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

Keyword

search

## Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	468656	4	138963972

## Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

Variable	Mean	SD	Min	Max
Age	34.2	10.5	20	55
Gender	Male	100%		
Marital status	Married	100%		
Education	High school	100%		
Occupation	Teacher	100%		
Income	Low	100%		
Religion	Islam	100%		
Health status	Good	100%		
Smoking status	Non-smoker	100%		
Alcohol consumption	None	100%		
Stress level	Low	100%		
Sleep quality	Good	100%		
Appetite	Good	100%		
Weight change	Stable	100%		
Blood pressure	Normal	100%		
Blood sugar	Normal	100%		
Cholesterol	Normal	100%		
Triglycerides	Normal	100%		
Hemoglobin A1c	Normal	100%		
Uric acid	Normal	100%		
Creatinine	Normal	100%		
Urea nitrogen	Normal	100%		
Calcium	Normal	100%		
Phosphorus	Normal	100%		
Magnesium	Normal	100%		
Potassium	Normal	100%		
Sodium	Normal	100%		
Iron	Normal	100%		
Zinc	Normal	100%		
Copper	Normal	100%		
Manganese	Normal	100%		
Selenium	Normal	100%		
Chromium	Normal	100%		
Cobalt	Normal	100%		
Nickel	Normal	100%		
Vanadium	Normal	100%		
Molybdenum	Normal	100%		
Fluorine	Normal	100%		
Iodine	Normal	100%		
Silicon	Normal	100%		
Boron	Normal	100%		
Strontium	Normal	100%		
Barium	Normal	100%		
Calcium	Normal	100%		
Phosphorus	Normal	100%		
Magnesium	Normal	100%		
Potassium	Normal	100%		
Sodium	Normal	100%		
Iron	Normal	100%		
Zinc	Normal	100%		
Copper	Normal	100%		
Manganese	Normal	100%		
Selenium	Normal	100%		
Chromium	Normal	100%		
Cobalt	Normal	100%		
Nickel	Normal	100%		
Vanadium	Normal	100%		
Molybdenum	Normal	100%		
Fluorine	Normal	100%		
Iodine	Normal	100%		
Silicon	Normal	100%		
Boron	Normal	100%		
Strontium	Normal	100%		
Barium	Normal	100%		
Calcium	Normal	100%		
Phosphorus	Normal	100%		
Magnesium	Normal	100%		
Potassium	Normal	100%		
Sodium	Normal	100%		
Iron	Normal	100%		
Zinc	Normal	100%		
Copper	Normal	100%		
Manganese	Normal	100%		
Selenium	Normal	100%		
Chromium	Normal	100%		
Cobalt	Normal	100%		
Nickel	Normal	100%		
Vanadium	Normal	100%		
Molybdenum	Normal	100%		
Fluorine	Normal	100%		
Iodine	Normal	100%		
Silicon	Normal	100%		
Boron	Normal	100%		
Strontium	Normal	100%		
Barium	Normal	100%		
Calcium	Normal	100%		
Phosphorus	Normal	100%		
Magnesium	Normal	100%		
Potassium	Normal	100%		
Sodium	Normal	100%		
Iron	Normal	100%		
Zinc	Normal	100%		
Copper	Normal	100%		
Manganese	Normal	100%		
Selenium	Normal	100%		
Chromium	Normal	100%		
Cobalt	Normal	100%		
Nickel	Normal	100%		

## Allele Sequence

Variation Type	:	SNP
Flanking Sequence	:	Information
5' Assay	:	TGGGCGCGGT
Observed	:	T/C
3' Assay	:	GAGGTGAGGA GATCGAGACC ACGATGAAC CCGCTCTCTA CTAAATAATAC AAAAAATATAG
Comment	:	repeat sequence (SNP is present in repeat sequence)
Sample size	:	96

## Screened Sequence

Accession No.	:	NT_006124.3	(Graphical View of this Entry)
Chromosome	:	4	
Map	:		
Definition of the record	:	Homo sapiens chromosome 4 working draft sequence segment.	
Position in Sequence	:	468642	(View SNP position in this record)

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID	:	NT_006124.3	20010416_6	
Amplified region	:	467851..468999	in NT_006124	
size	:	1149		
Pre-Denature	:	94.0 degrees	C for	2.00 minutes
Denaturation	:	94.0 degrees	C for	0.50 minutes

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105126](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105126)

12/17/2001

# PCR "CEBCT"

Annealing : 60.0 degrees C for 0.50 minutes  
 Polymerization : 72.0 degrees C for 2.00 minutes  
 PCR Cycles : 35  
 Post-Extension : 72.0 degrees C for 7.00 minutes  
 ForwardPrimer : GCAGTGCAGT TTGGACTTAG  
 BackwardPrimer : GAAAGACATG GCTGAGGTAG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

# SNP Information for IMS-JST105129

## General Information

JSNP ID : IMS-JST105129  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(7):385-407  
Release Date : 2001/08/09  
Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	466132	4	138966496

## Gene Information

### Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105129](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105129)

12/17/2001

Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CTACCAATCC TGGAGACTAA AAAAAATAAA CAGTGTGTGC ATCAGAGTGC TATGTTGCAG  
Observed : A/G  
3' Assay : TATATGAACT TTGGCTTCAT TCTAATTTAA TTCAATAATG AAAAAAATAT TGAGACAAAC  
Comment :  
Sample size : 96

Screened Sequence

Accession No. : NT\_006124.3 (Graphical View of this Entry)  
Chromosome : 4  
map :  
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.  
Position in Sequence : 466118 (View SNP position in this record)

Method

PCR Method  
Sequence Method

PCR Profile

Screening region ID : NT\_006124.3.20010416.7  
Amplified region : 466019..467240 in NT\_006124  
size : 1222  
Pre-Denature : 94.0 degrees C for 2.00 minutes  
Denaturation : 94.0 degrees C for 0.50 minutes

--- SNP INFORMATION ---

PCR REACTION

Annealing : 60.0 degrees C for 0.50 minutes  
Polymerization : 72.0 degrees C for 2.00 minutes  
PCR Cycles : 35  
Post-Extension : 72.0 degrees C for 7.00 minutes  
ForwardPrimer : ACGTCTTCTA TGAATAGAGG C  
BackwardPrimer : AAGCTCATGT CGTTCATTT C



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-IST105129](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105129)

12/17/2001

# SNP Information for IMS-JST105136

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

## General Information

JSNP ID : IMS-JST105136  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HCBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004648.5	2300671	1	165016888

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : AAATTAGCA GTTAGCAGCA AGTAGATTAT CGCTATGTAA AATAAAATTC CTGAGTTTCT

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105136](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105136)

12/17/2001



# Sequence

Observed : G/C  
3' Assay : TCACTCGCTC TTACAGTACC TACCTGCCTA CCTGCCTCTG AGGAGAAACG CTGTAATTAG  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_004648.3 (Graphical View of this Entry)  
Chromosome : 1  
map  
Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.  
Position in Sequence : 422012 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_004648.3 20010416\_3  
Amplified region : 421033..422147 in NT\_004648  
size : 1115

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes

ForwardPrimer : CGAAGAATAT ACTGCTACGG T

Forward Primer : CACCTGACAT C

BackwardPrimer : AGTTTGACCA CACCTGACAT C



12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105136](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105136)

# SNP Information for IMS-JST105137

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

## General Information

JSNP ID : IMS-JST105137  
 dbSNP ID(rs#) :  
 dbSNP ID(ss#) :  
 HCBASE ID :  
 Organism : Homo sapiens  
 Molecular type : Genomic  
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
 Citation : J Hum Genet. 2001;46(7):385-407  
 Release Date : 2001/08/09  
 Last Update : 2001/08/09

Keyword

search

## Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004648.5	2300743	1	165016960

## Gene Information

## Allele Sequence

Variation Type : SNP  
 Flanking Sequence Information  
 5' Assay : TACAGTACCT ACCTGCCTAC CTGCCTCTGA GGAGAAACGC TGTAAATTAGG CAACAGGAAA

12/17/2001

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105137](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105137)

Observed : A/G  
 3' Assay : TTGTACTATC TTTCAAATGC ATTTGCAAT GCCTTTAAGG ATTTTATCCT TTAGAATCAT  
 Comment :  
 Sample size : 96

## Screened Sequence

Accession No. : NT\_004648.3 (Graphical View of this Entry)  
 Chromosome : 1  
 map  
 Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.  
 Position in Sequence : 421940 ([View SNP position in this record](#))

## Method

PCR Method  
Sequence Method

## PCR Profile

Screening region ID : NT\_004648.3 20010416\_3  
 Amplified region : 421033..422147 in NT\_004648  
 size : 1115

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CGAAGAATAT ACTGCTACGG	T



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075388

General Information

JSNP ID : IMS-JST075388  
dbSNP ID(rs#) :  
dbSNP ID(ss#) :  
HGBASE ID :  
Organism : Homo sapiens  
Molecular type : Genomic  
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN  
Citation : J Hum Genet. 2001;46(4):225-40  
Release Date : 2001/06/11  
Last Update : 2001/06/11

Keyword

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	334554	22	40632693

Gene Information

Locus Link ID : 25830  
Gene Name : sulfortranferase family 4A, member 1  
Gene symbol : SULT4A1  
Alias symbol : SULTX3, BR-STL-1, DJ388M5.3  
Product : sulfortranferase family 4A, member 1

Relation to gene sources

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST075388](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075388)

12/17/2001

NT_011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology 25830

view predicted exons with Unigene : [Hs.189810](#)

## Allele Sequence

Variation Type : SNP  
Flanking Sequence Information  
5' Assay : CAGTGTGACT GTGTATGGT TAGCAGGGAG CGGCTCCTA GCCTGGGCTT CTGGAGGGAG  
Observed : C/T  
3' Assay : GAGAGGAGAG TGGAGGGCCC ATTGAGAGGT GGAAGCCTCC CTAAGCATG CTTTGGAGAC  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : [NT\\_011521.1](#) ([Graphical View of this Entry](#))  
Chromosome : 22  
map :  
Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.  
Position in Sequence : 334554 ([View SNP position in this record](#))

## Method

[PCR Method](#)  
[Sequence Method](#)

NT\_011521.1 20010416\_4

## PCR Profile

Screening region ID : NT\_011521.1 20010416\_4  
Amplified region : 334027..335031 in NT\_011521  
size : 1005

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TAGGTCTCGA GAAGAGCCTG T	
BackwardPrimer	:	GCATCAGCAG CAGCGACGAT G	







TOGETHER

Observed : G/C  
3' Assay : ACTCTCTGCC ACTTTCTGTT GCTGGCCTTG TCTGTCTGGA GGAAGGAGGA GGGTAGATTA  
Comment :  
Sample size : 96

## Screened Sequence

Accession No. : NT\_019583.3 (Graphical View of this Entry)  
Chromosome : 14  
map  
Definition of the record : Homo sapiens chromosome 14 working draft sequence segment.  
Position in Sequence : 3336512 ([View SNP position in this record](#))

## Method

PCR Method  
[Sequence Method](#)

## PCR Profile

Screening region ID : NT\_019583.3.20010417\_3  
Amplified region : 3335968..3337267 in NT\_019583  
size : 1300

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AGCTGTAACA CTCACTGCCGA	

[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP\\_ID=IMS-JST105400](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105400)

12/17/2001

TGAGTTCGCGGT

BackwardPrimer : GTGCGTTCAT GGTCTCAGGA

